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 M I S R L H  
 \*\*\*\*\* (TM)  
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MPSrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jan 21 14:30:17 2000; MasPar time 6.36 Seconds

Tabular output not generated. 330.840 Million cell updates/sec

Title: >US-09-176-546-2

Description: (1-99) from US09176546.pap

Perfect Score: 682

Sequence: 1 MADGSSDAAREPRAPAPAPR.....CQPLELAGLGFALQLDLCRQ 99

Scoring table: PAM 150

Gap 11

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

a-geneseq35

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
 14:part14 15:part15 16:part16 17:part17 18:part18  
 19:part19 20:part20 21:part21 22:part22 23:part23  
 24:part24 25:part25 26:part26 27:part27 28:part28  
 29:part29 30:part30 31:part31 32:part32 33:part33  
 34:part34 35:part35 36:part36 37:part37 38:part38  
 39:part39

Statistics: Mean 28.682; Variance 122.478; scale 0.234

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	ID	Description	Pred. No.
1	682	100.0	216 37 W2758	Modified human cardia	7.11e-55
2	682	100.0	216 29 W41573	Modified human cardia	7.11e-55
3	682	100.0	222 29 W41570	Modified human cardia	7.11e-55
4	680	99.7	226 26 W18054	Recombinant human myo	1.12e-54
5	678	99.4	319 29 W41572	Human cardiac troponin	1.75e-54
6	678	99.4	372 29 W41571	Cardiac troponin I/c	1.75e-54
7	659	98.1	153 26 W18053	Recombinant myofibril	1.34e-53
8	536	78.6	80 21 W02286	Human troponin I frag	1.28e-40
9	239	35.0	38 12 W61181	Cardiac troponin I	2.16e-12
10	233	34.2	35 21 W02285	Human troponin I frag	7.62e-12
11	207	30.4	31 32 W37924	N-terminal amino acid	1.73e-09
12	202	29.6	30 11 R52781	Human cardiac troponi	4.88e-09
13	202	29.6	31 21 W05041	N-terminus of cardiac	4.88e-09
14	202	29.6	31 14 R73052	N-terminal sequence o	4.88e-09
15	201	29.5	182 26 W22598	Human fast twitch ske	5.99e-09
16	173	25.4	26 11 R55786	Human cardiac troponi	1.83e-06

17 139 20.4 24 11 R66736 Synthetic immunogen b 1.56e-03  
 18 129 18.9 39 12 R66183 Cardiac troponin I pe 1.08e-02  
 19 127 18.6 39 32 W65159 Synthetic bi-epitopic 1.58e-02  
 20 126 18.5 38 32 W65160 Synthetic bi-epitopic 1.91e-02  
 21 112 16.4 35 32 W65158 Synthetic bi-epitopic 2.66e-01  
 22 110 16.1 33 32 W65157 Synthetic bi-epitopic 3.84e-01  
 23 104 15.2 24 32 W65161 Synthetic bi-epitopic 1.15e+00  
 24 103 15.1 20 25 W30854 Human cardiac troponi 1.38e+00  
 25 101 14.8 258 26 W22599 Human fast twitch ske 1.99e+00  
 26 100 14.7 28 32 W65156 Synthetic bi-epitopic 2.38e+00  
 27 100 14.7 29 32 W65162 Synthetic bi-epitopic 2.38e+00  
 28 94 13.8 374 2 P80277 Sequence encoded by 3 6.93e+00  
 29 93 13.6 27 32 W65155 Synthetic bi-epitopic 8.27e+00  
 30 92 13.5 111 1 P81515 Bovine Bone Morphogen 9.86e+00  
 31 87 12.8 716 1 P81099 Sequence of Rhodospir 2.35e+01  
 32 87 12.8 716 1 P83141 Sequence of L-phenyla 2.35e+01  
 33 87 12.8 716 13 R70682 Stabilised phenylalan 2.35e+01  
 34 87 12.8 716 1 P80513 L-phenylalanine ammon 2.35e+01  
 35 87 12.8 716 1 P95783 L-phenylalanine ammon 2.79e+01  
 36 86 12.6 13 12 R66182 Cardiac troponin I pe 2.79e+01  
 37 85 12.5 657 6 R29580 FMR-1 gene product.. 3.31e+01  
 38 84 12.3 183 39 W89689 Murine osteogenic pro 3.93e+01  
 39 84 12.3 183 12 R51643 Mature mouse CBMP3. 3.93e+01  
 40 84 12.3 183 8 R44756 Murine osteogenic pro 3.93e+01  
 41 84 12.3 183 16 R85764 Mature murine CBMP3. 3.93e+01  
 42 84 12.3 183 29 W44312 Murine osteogenic pro 3.93e+01  
 43 84 12.3 432 13 R77865 S. clavuligerus ORF8 3.93e+01  
 44 84 12.3 436 21 W03662 Human 70K UI snRNP pr 3.93e+01  
 45 84 12.3 614 15 R82630 70K autoantigen, part 3.93e+01

#### ALIGNMENTS

RESULT 1

ID W2758 standard; Protein; 216 AA.

AC W2758;

DT 13-JAN-1999 (first entry)

DE Modified human cardiac troponin I.

KW Human cardiac troponin I; troponin I.

KW stable troponin subunit; cardiac disorder; myocardial damage;

KW heart attack.

OS Homo sapiens.

OS Synthetic.

PN US5834210-A.

PD 10-NOV-1998.

PF 31-OCT-1997; 961858.

PR 31-OCT-1997; US-961858.

PR 23-MAY-1997; US-862613.

PR (SPEPC-) SPECTRAL DIAGNOSTICS INC.

PI Liu S, Shi Q.

DR WPI: 99-008702/01.

DR N-PSDB; V67262.

PT Recombinant modified human cardiac troponin I and complexes with

troponin T and C - for use in assays to determine levels of these

proteins, as control values in determining extent of cardiac damage

PT e.g. in heart attacks

PS Claim 2; Fig 1; 16pp; English.

CC The present sequence represents modified human cardiac troponin I.  
 CC Expression in Escherichia coli of the modified troponin I is increased  
 CC compared to that of the native sequence. The modified troponin I  
 CC consists of the native troponin I protein sequence with an N-terminal  
 CC extension of 5-8 residues, including an N-terminal methionine. The  
 CC present invention describes troponin protein complexes which are useful  
 CC for the determination of myocardial damage. Troponin I and troponin T  
 CC have been found to be highly specific markers for cardiac disorders,  
 CC especially heart attacks. They must be complexed with troponin C to form  
 CC a stable structure, which is difficult to isolate. Recombinant  
 CC preparation of the trimeric structure allows sufficient quantities to be  
 CC obtained, so that assays can be performed to accurately determine  
 CC quantification of troponin complex levels for e.g. control values. The  
 CC complex can also be used as an antigen to raise antibodies.  
 SQ Sequence 216 AA;

Query Match 100.0%; Score 682; DB 37; Length 216;  
 Best Local Similarity 100.0%; Pred. No. 7.11e-55;  
 Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Dd 7 madgssdaareppapapirrrssnyrayatephakkskissarklqkltlllqakqe 66  
 Qy 1 MADGSSDAAREPPAPAPIRRRSSNYRAYATEPHAKKSKISASRKLQKLTLLQIAKQE 60

Dd 67 lereaeergerkgralstrcqpelaglgfaelqdlcrq 105  
 Qy 61 LEREAEERGERKGRALSTRCQPLELAGLGFAELQDLCRQ 99

## RESULT 2

ID W41573 standard; Protein: 216 AA.

AC W41573;

DT 22-JUN-1998 (first entry)

DE Modified human cardiac troponin I HcTnI-(HL)3.

KW Troponin I; immunoassay; assay; analysis; human; cardiac muscle;

KW skeletal muscle; injury; myocardial infarction; diagnosis;

KW HcTnI-(HL)3.

OS Homo sapiens.

OS Synthetic.

PH Key Location/Qualifiers

FT Protein 1-210

FT Peptide /label= HcTnI

FT 211..216

FT /label= (HL)3

FT /note= "(Claim 23)"

PN W09739132-A1.

PD 23-OCT-1997.

PF 14-APR-1997; U06147.

PR 11-APR-1997; US-833743.

PR 16-APR-1996; US-015772.

PA (UYMI-) UNIV MIAMI.

PI Potter JD;

DR WPI; 98-062676/06.

DR N-PSDB; V04230.

PT Immunoassay of mammalian troponin using stable standard for comparison - specifically acid-dialysed solution or its lyophilisate used for diagnosis of cardiac or skeletal muscle damage

PS Example 5; Page 74-75; 94pp; English.

CC This polypeptide comprises a C-terminally modified cardiac troponin I protein, designated HcTnI-(HL)3, comprising human cardiac troponin I (HcTnI) modified to add an alternating 3 histidine 3 leucine tag (see W41569). This modification alters the isoelectric point of

CC the protein, thereby improving its solubility and stability. A polynucleotide (see V04230) encoding the modified HcTnI was produced by PCR amplification of a HcTnI cDNA template, and was inserted into

CC vector pET lld to allow expression of HcTnI-(HL)3 in Escherichia coli transformants. The invention provides an assay for measuring

CC mammalian, preferably human, troponin in a patient sample. The

CC assay involves comparing the level in the sample with a novel troponin protein standard. This is a storage stable, soluble

CC troponin, a functional fragment of the troponin, a modified troponin or its functional fragment, a troponin fusion protein or a hetero-

CC multimeric troponin complex (see W41570-75). The method is used to monitor changes in the level of human troponin, particularly for

CC diagnosis of diseases involving damage to heart or skeletal muscle,

CC e.g. acute myocardial infarction. It may also be used to study

CC normal and pathological functions of troponin-expressing tissues.

SQ Sequence 216 AA;

Query Match 100.0%; Score 682; DB 29; Length 216;

Best Local Similarity 100.0%; Pred. No. 7.11e-55;

Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Dd 1 madgssdaareppapapirrrssnyrayatephakkskissarklqkltlllqakqe 60  
 Qy 1 MADGSSDAAREPPAPAPIRRRSSNYRAYATEPHAKKSKISASRKLQKLTLLQIAKQE 60

Dd 61 lereaeergerkgralstrcqpelaglgfaelqdlcrq 99

Qy 61 LEREAEERGERKGRALSTRCQPLELAGLGFAELQDLCRQ 99

## RESULT 3

ID W41570 standard; Protein: 222 AA.

AC W41570;

DT 22-JUN-1998 (first entry)

DE Modified human cardiac troponin I HcTnI-K6-H5-D.

KW Troponin I; immunoassay; assay; analysis; human; cardiac muscle;

KW skeletal muscle; injury; myocardial infarction; diagnosis;

KW HcTnI-K6-H5-D.

OS Homo sapiens.

OS Synthetic.

PN W09739132-A1.

PD 23-OCT-1997.

PF 14-APR-1997; U06147.

PR 11-APR-1997; US-833743.

PR 16-APR-1996; US-015772.

PA (UYMI-) UNIV MIAMI.

PI Potter JD;

DR WPI; 98-062676/06.

DR N-PSDB; V04221.

PT Immunoassay of mammalian troponin using stable standard for

PT comparison - specifically acid-dialysed solution or its lyophilisate

PT used for diagnosis of cardiac or skeletal muscle damage

PS Example 2; Page 64-65; 94pp; English.

CC This polypeptide comprises a C-terminally modified cardiac troponin I protein, designated HcTnI-K6-H5-D, comprising human cardiac troponin I (HcTnI) modified to add 6 lysines, 5 histidines and one aspartate residue. This modification was made to alter the isoelectric point

CC of the protein, thereby improving its solubility and stability. A polynucleotide (see V04221) encoding the modified HcTnI was produced

CC by PCR amplification of a HcTnI cDNA template, and was inserted into vector pET lld to allow expression of HcTnI-K6-H5-D in Escherichia

CC coli transformants. The invention provides an assay for measuring mammalian, preferably human, troponin in a patient sample. The

CC assay involves comparing the level in the sample with a novel troponin protein standard. This is a storage stable, soluble

CC troponin, a functional fragment of the troponin, a modified troponin or its functional fragment, a troponin fusion protein or a hetero-

CC multimeric troponin complex (see W41570-75). The method is used to monitor changes in the level of human troponin, particularly for

CC diagnosis of diseases involving damage to heart or skeletal muscle, e.g. acute myocardial infarction. It may also be used to study

CC normal and pathological functions of troponin-expressing tissues.

SQ Sequence 222 AA;

Query Match 100.0%; Score 682; DB 29; Length 222;  
 Best Local Similarity 100.0%; Pred. No. 7.11e-55;  
 Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Dd 1 madgssdaareppapapirrrssnyrayatephakkskissarklqkltlllqakqe 60  
 Qy 1 MADGSSDAAREPPAPAPIRRRSSNYRAYATEPHAKKSKISASRKLQKLTLLQIAKQE 60

Dd 61 lereaeergerkgralstrcqpelaglgfaelqdlcrq 99

## RESULT 4

ID W18054 standard; protein: 226 AA.

AC W18054;

DT 20-FEB-1998 (first entry)

DE Recombinant human myofibrillar contractile protein Troponin I.

KW Cardiac isotype; myofibrillar contractile protein; Troponin I; cTnI; inhibitory subunit; thin filament regulatory protein; TnI immunoassay;

KW calcium sensitivity; cardiac muscle; striated muscle;

KW degradation product; cyanogen bromide cleavage; myocardial infarction;

KW immunological activity.

OS Synthetic.

OS Homo sapiens.

PH Key Location/Qualifiers

FT Modified\_site 87 /note= "carboxymethylated to prevent dimerisation by  
 FT FT inter or intra disulphide bridges"  
 FT Modified\_site 104 /note= "carboxymethylated to prevent dimerisation by  
 FT FT inter or intra disulphide bridges"  
 FT Peptide 9..217 /note= "human Troponin I"  
 FT FT /note= "CN-Br cleavage fragment"  
 FT Peptide 9..161 /note= "CN-Br cleavage fragment"  
 FT FT /note= "CN-Br cleavage fragment"  
 FT Peptide 8..219 /note= "CN-Br cleavage fragment"  
 FT FT /note= "CN-Br cleavage fragment"  
 FT Peptide 2..4 /note= "CN-Br cleavage fragment"  
 FT FT /note= "CN-Br cleavage fragment"  
 FT Peptide 5..8 /note= "CN-Br cleavage fragment"  
 FT FT /note= "CN-Br cleavage fragment"  
 FT Peptide 163..208 /note= "CN-Br cleavage fragment"  
 FT FT /note= "CN-Br cleavage fragment"  
 FT Peptide 209..119 /note= "CN-Br cleavage fragment"  
 FT FT /note= "CN-Br cleavage fragment"  
 FT Peptide 220..226 /note= "CN-Br cleavage fragment"  
 FT FT /note= "CN-Br cleavage fragment"  
 FT Peptide 14..101 /note= "CN-Br cleavage fragment"  
 FT FT /note= "CN-Br cleavage fragment"  
 PN WO9719955-A1.  
 PD 05-JUN-1997.  
 PF 26-NOV-1996; U18878.  
 PR 29-NOV-1995; US-564526.  
 PA (DADE-) DADE INT INC.  
 PI Demarco C, Morjana NA;  
 DR WPI: 97-310526/28.  
 PT Human cardiac Troponin I cyanogen bromide cleaved fragment - used in  
 PT calibrator or control for troponin I immunoassay  
 PS Disclosure: Page 20; 52pp; English.  
 CC The present sequence represents a recombinant form of the cardiac  
 CC isotype of the myofibrillar contractile protein Troponin I (cTnI).  
 CC Troponin I is the inhibitory subunit of Troponin, a thin filament  
 CC regulatory protein complex which confers calcium sensitivity to the  
 CC cardiac and striated muscle. cTnI was cleaved with cyanogen bromide,  
 CC which cleaves at Met residues with a high specificity under acidic  
 CC conditions, to generate several fragments. A 153 amino acid CNBr-cTnI  
 CC isoform is used in a calibrator or a control for a TnI immunoassay. The  
 CC CNBr-cTnI isoform is comparable in molecular weight to a major  
 CC degradation product of native cTnI in the serum of patients who have  
 CC experienced myocardial infarction. The peptide has immunological activity  
 CC to antibodies against TnI. The CNBr-cTnI isoform has an average of 3-4  
 CC times more reactivity than TnI and lower non-specific binding, as  
 CC measured by radial partition immunoassay. It also has increased stability  
 CC over the synthetic peptide currently used in the Dade TnI immunoassay.  
 SQ Sequence 226 AA;

Query Match 99.7%; Score 680; DB 26; Length 226;  
 Best Local Similarity 99.0%; Pred. No. 1.12e-54;  
 Matches 98; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Db 8 madgssdaareppapaparrssnyravatephakkkisarklqltlllqakqe 67  
 QY 1 MADGSSDAREPPAPAPARRSSNRYATPEPHAKKSKISARKLQLTLLQIAKQE 60  
 Db 68 lereaeerrgekgalstrcqpeltglgfaelqdlcrq 106  
 QY 61 LEREAEERGERGKALSTRCPLELAGLGFALQDLQCRQ 99

RESULT 5  
 ID W41572 standard; Protein; 319 AA.  
 AC W41572;  
 DT 22-JUN-1998 (first entry)  
 DE Human cardiac troponin I/carp parvalbumin fusion protein.  
 KW Troponin I; parvalbumin; immunoassay; assay; analysis; human;  
 KW cardiac muscle; skeletal muscle; injury; myocardial infarction;  
 KW diagnosis; HcTnI; carp.  
 OS Chimeric - Homo sapiens.

OS Chimeric - Cyprinus carpio.  
 FH Key Location/Qualifiers  
 FT Protein 1..210  
 FT /label= HcTnI  
 FT 211..319  
 FT /label= Parvalbumin  
 PN WO9739132-A1.  
 PD 23-OCT-1997.  
 PF 14-APR-1997; U06147.  
 PR 11-APR-1997; US-833743.  
 PR 16-APR-1996; US-015772.  
 PA (UYMI-) UNIV MIAMI.  
 PI Potter JD;  
 DR WPI: 98-062676/06.  
 DR N-PSDB: V04228.  
 PT Immunoassay of mammalian troponin using stable standard for  
 PT comparison - specifically acid-dialysed solution or its lyophilisate  
 PT used for diagnosis of cardiac or skeletal muscle damage  
 PS Example 4; Page 71-72; 94pp; English.  
 CC This polypeptide comprises fusion protein with the N-terminal  
 CC region being human cardiac troponin I (HcTnI) and the C-terminal  
 CC region being carp parvalbumin. It was expressed in E. coli host  
 CC cells utilising a vector incorporating a polynucleotide (see  
 CC V04228) encoding the fusion. The addition of parvalbumin, a  
 CC calcium binding protein, to HcTnI provides more favourable solubility  
 CC properties to HcTnI and to the fusion protein. The invention  
 CC provides an assay for measuring mammalian, preferably human,  
 CC troponin in a patient sample. The assay includes the step of  
 CC comparing the level in the sample with a novel troponin protein  
 CC standard. This may be a storage stable, soluble mammalian troponin,  
 CC a functional fragment of the troponin, a modified troponin or its  
 CC functional fragment, a troponin fusion protein or a heteromultimeric  
 CC troponin complex (see also W41570-75). The method is used to  
 CC monitor changes in the level of human troponin, particularly for  
 CC diagnosis of diseases involving damage to heart or skeletal muscle,  
 CC e.g. acute myocardial infarction. It may also be used to study  
 CC normal and pathological functions of troponin-expressing tissues.  
 SQ Sequence 319 AA;

Query Match 99.4%; Score 678; DB 29; Length 319;  
 Best Local Similarity 99.0%; Pred. No. 1.75e-54;  
 Matches 98; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Db 1 mvdgssdaareppapaparrssnyravatephakkkisarklqltlllqakqe 60  
 QY 1 MADGSSDAREPPAPAPARRSSNRYATPEPHAKKSKISARKLQLTLLQIAKQE 60  
 Db 61 lereaeerrgekgalstrcqpeltglgfaelqdlcrq 99  
 QY 61 LEREAEERGERGKALSTRCPLELAGLGFALQDLQCRQ 99

RESULT 6  
 ID W41571 standard; Protein; 372 AA.  
 AC W41571;  
 DT 22-JUN-1998 (first entry)  
 DE Cardiac troponin I/cardiac troponin C fusion protein.  
 KW Troponin I; troponin C; immunoassay; assay; analysis; human;  
 KW cardiac muscle; skeletal muscle; injury; myocardial infarction;  
 KW diagnosis; HcTnI; HcTnC.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT Protein 1..210  
 FT /label= HcTnI  
 FT 211..372  
 FT /label= HcTnC  
 PN WO9739132-A1.  
 PD 23-OCT-1997.  
 PF 14-APR-1997; U06147.  
 PR 11-APR-1997; US-833743.  
 PR 16-APR-1996; US-015772.  
 PA (UYMI-) UNIV MIAMI.  
 PI Potter JD;

DR WPI; 98-062676/06.  
 DR N-PSDB; V04225.  
 PT Immunassay of mammalian troponin using stable standard for  
 PT comparison - specifically acid-dialysed solution or its lyophilisate  
 PT used for diagnosis of cardiac or skeletal muscle damage  
 PS Example 3; Page 67-68; 94pp; English.  
 CC This protein sequence comprises a fusion protein with the  
 CC N-terminal region being human cardiac troponin I (HcTnI) and  
 CC the C-terminal region being human cardiac troponin C (HcTnC). It  
 CC has been expressed in E. coli host cells utilising a vector  
 CC carrying a HcTnI-HcTnC polynucleotide (see V04225) obtained by PCR.  
 CC The addition of the calcium binding protein HcTnC to HcTnI provided  
 CC more favourable solubility properties to HcTnI. The invention  
 CC provides an assay for measuring mammalian, preferably human,  
 CC troponin in a patient sample. The assay includes the step of  
 CC comparing the level in the sample with a novel troponin protein  
 CC standard. This may be a storage stable, soluble mammalian troponin,  
 CC a functional fragment of the troponin, a modified troponin or its  
 CC functional fragment, a troponin fusion protein or a heteromultimeric  
 CC troponin complex (see also W41570-75). The method is used to  
 CC monitor changes in the level of human troponin, particularly for  
 CC diagnosis of diseases involving damage to heart or skeletal muscle,  
 CC e.g. acute myocardial infarction. It may also be used to study  
 CC normal and pathological functions of troponin-expressing tissues.  
 SQ Sequence 372 AA;

Query Match 99.4%; Score 678; DB 29; Length 372;  
 Best Local Similarity 99.0%; Pred. No. 1.75e-54;  
 Matches 98; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 mvdgsdaareprpapapirrrssnyrayatephakkkksasrkqlklllqiaqke 60  
 QY 1 MADGSSDAAREPRPAPAPIRRRSSNYRAYATEPHAKKKKSASRKQLKLLQLIAQKE 60

Db 61 lereeergerkgralstrcqpelaglgfaelqdlcrq 99  
 QY 61 LEREERGERGKRALSTRCQPLEAGLGFAELQDLCRQ 99

RESULT 7  
 ID W18053 standard; protein; 153 AA.  
 AC W18053;  
 DE Recombinant myofibrillar contractile protein Troponin I CN-Br fragment.  
 KW Cardiac isotype; myofibrillar contractile protein; Troponin I; ctni;  
 KW inhibitory subunit; thin filament regulatory protein; Tni immunoassay;  
 KW calcium sensitivity; cardiac muscle; striated muscle;  
 KW degradation product; cyanogen bromide cleavage; myocardial infarction;  
 KW immunological activity.  
 OS Synthetic.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT Modified\_site 79  
 FT /note= "carboxymethylated to prevent dimerisation by  
 FT inter or intra disulphide bridges"  
 FT Modified\_site 96  
 FT /note= "carboxymethylated to prevent dimerisation by  
 FT inter or intra disulphide bridges"  
 FT W09719955-Al.  
 PN 05-JUN-1997.  
 PF 26-NOV-1996; U18878.  
 PR 29-NOV-1995; US-564526.  
 PA (DADE-) DADE INT INC.  
 PI Demarco C, Morjana NA;  
 DR WPI; 97-310526/28.  
 PT Human cardiac Troponin I cyanogen bromide cleaved fragment - used in  
 PT calibrator or control for troponin I immunoassay  
 PS Disclosure; Page 20; 52pp; English.  
 CC The present sequence represents a CN-Br cleavage fragment of the  
 CC recombinant cardiac isotype of the myofibrillar contractile protein  
 CC Troponin I (ctni). Troponin I is the inhibitory subunit of troponin,  
 CC a thin filament regulatory protein complex which confers calcium  
 CC sensitivity to the cardiac and striated muscle. The present 153 amino

CC acid CNBr-ctni isoform is used in a calibrator or a control for a Tni  
 CC immunoassay. The CNBr-ctni isoform is comparable in molecular weight to  
 CC a major degradation product of native ctni in the serum of patients who  
 CC have experienced myocardial infarction. The peptide has immunological  
 CC activity to antibodies against Tni. The CNBr-ctni isoform has an average  
 CC of 3-4 times more reactivity than rTni and lower non-specific binding, as  
 CC measured by radial partition immunoassay. It also has increased stability  
 CC over the synthetic peptide currently used in the bade Tni immunoassay.  
 SQ Sequence 153 AA;

Query Match 98.1%; Score 669; DB 26; Length 153;  
 Best Local Similarity 99.0%; Pred. No. 1.34e-53;  
 Matches 97; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 adgssdaareprpapapirrrssnyrayatephakkkksasrkqlklllqiaqkel 60  
 QY 2 ADGSSDAAREPRPAPAPIRRRSSNYRAYATEPHAKKKKSISASRKQLKLLQLIAQKEL 61

Db 61 ereaeergerkgralstrcqpelaglgfaelqdlcrq 98  
 QY 62 EREAERGERGKRALSTRCQPLEAGLGFAELQDLCRQ 99

RESULT 8  
 ID W02286 standard; peptide; 80 AA.  
 AC W02286;  
 DE 27-MAY-1997 (first entry)  
 DE Human troponin I fragment, residues 2-81 (initial Met is residue 1).  
 KW Cardiac; heart; troponin I; fragment; analyte; aqueous calibrator;  
 KW stabiliser; myosin; myoglobin; lactate dehydrogenase; creatine kinase;  
 KW myocardial infarction; heart attack.  
 OS Homo sapiens.  
 PN W09627661-Al.  
 PD 12-SEP-1996.  
 PF 06-MAR-1996; U03034.  
 PR 07-MAR-1995; US-400158.  
 PA (DADE-) DADE INT INC.  
 PI Bauer R, Chin B, Flaa C, Sabucedo A;  
 DR WPI; 96-425423/42.  
 PT Ag. compsn. for stabilising proteins for use as controls for cardiac  
 PT markers - comprising buffer, reducing agent, stabilising protein,  
 PT chelating agent and salt  
 PS Claim 6; Page 41; 57pp; English.  
 CC W02285 and W02286 are troponin I fragments used to exemplify the  
 CC usefulness of an aqueous composition (may be lyophilised) used as an  
 CC aqueous calibrator and control solution for diagnostic assays for  
 CC cardiac proteins and peptides. The stabilising solution comprises a  
 CC buffer, a reducing agent (e.g. 2-mercaptoethanol or N-acetyl-cysteine),  
 CC a stabilising protein (e.g. albumin or casein), a chelating agent (e.g.  
 CC EDTA or EGTA) a salt (e.g. NaCl), a blocking agent (especially gelatin)  
 CC and a bulking agent (e.g. trehalose, glucose, sucrose, galactose, etc.)  
 CC The composition is especially useful for diagnostic assays of  
 CC troponin, myoglobin, creatine kinase (CK), CK isoenzymes, lactate  
 CC dehydrogenase (LD), LD isoenzymes, myosin and fragments of these. The  
 CC composition may be used, e.g. in tests for acute myocardial infarction.  
 CC The stabilising composition is not derived from human serum, and thus  
 CC prevents exposure of the user (and manufacturing personnel) to many of  
 CC the diseases which can be spread by contact with human blood products.  
 CC The composition is also able to keep analytes stable in liquid form for  
 CC extended periods of time.  
 SQ Sequence 80 AA;

Query Match 78.6%; Score 536; DB 21; Length 80;  
 Best Local Similarity 100.0%; Pred. No. 1.28e-40;  
 Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 adgssdaareprpapapirrrssnyrayatephakkkksasrkqlklllqiaqkel 60  
 QY 2 ADGSSDAAREPRPAPAPIRRRSSNYRAYATEPHAKKKKSISASRKQLKLLQLIAQKEL 61

Db 61 ereaeergerkgralstrcqpelaglgfaelqdlcrq 80  
 QY 62 EREAERGERGKRALSTRCQ 81

CC the diseases which can be spread by contact with human blood products.  
 CC The composition is also able to keep analytes stable in liquid form for  
 CC extended periods of time.

# RESULT 9

ID R66181 standard; peptide: 38 AA.  
 AC R66181;  
 DT 21-JUL-1995 (first entry)  
 DE Cardiac troponin I peptide fragment #1.  
 KW Cardiac troponin I; skeletal troponin I; immunoassay; antibody;  
 KW myocardial damage; myocardial infarction.  
 OS Synthetic.  
 PN WO9427156-A.  
 PD 24-NOV-1994.  
 PF 16-MAY-1994; U05468.  
 PR 17-MAY-1993; US-063168.  
 PA (FORT-) FORTON BIOSCIENCE INC.  
 PI Torretti SA, Vargas AM, Wicks RW, Zartman LO;  
 DR WPI: 95-006973/01.  
 PT Quantitative assay of cardiac troponin I - for diagnosis of  
 PT myocardial damage, esp. infarction, also new antibodies specific  
 PT for cardiac but not skeletal troponin I  
 PS Claim 12; Page 21; 31pp; English.  
 CC The sequences given in R66181-83 represent peptides which are  
 CC derived from cardiac troponin I but which are not present in skeletal  
 CC troponin I. These peptides may be used in an immunoassay for the  
 CC quantitation of cardiac troponin I in a biological fluid. These  
 CC peptides bind antibodies specific for cardiac troponin I and may be  
 CC used to confirm diagnosis of myocardial damage, esp. myocardial  
 CC infarction.  
 SQ Sequence 38 AA;

Query Match 35.0%; Score 239; DB 12; Length 38;  
 Best Local Similarity 97.4%; Pred. No. 2.16e-12;  
 Matches 38; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Db 1 madgssdaareppapapirrrssnyrayatephakhs 38

QY 1 MADGSSDAAREPPAPAPIRRRSSNYRAYATEPHAKHS 39

# RESULT 10

ID W02285 standard; peptide: 35 AA.  
 AC W02285;  
 DT 27-MAY-1997 (first entry)  
 DE Human troponin I fragment, residues 27-61 (initial Met is residue 1).  
 KW Cardiac; heart; troponin I; fragment; analyte; aqueous calibrator;  
 KW stabiliser; myosin; myoglobin; lactate dehydrogenase; creatine kinase;  
 KW myocardial infarction; heart attack.  
 OS Homo sapiens.  
 PN WO9627661-A1.  
 PD 12-SEP-1996.  
 PF 06-MAR-1996; U03034.  
 PR 07-MAR-1995; US-400158.  
 PA (DADE-) DADE INT INC.  
 PI Bauer, R, Chin B, Flaa C, Sabucedo A;  
 DR WPI: 96-425423/42.  
 PT Aq. compsn. for stabilising proteins for use as controls for cardiac  
 PT markers - comprising buffer, reducing agent, stabilising protein,  
 PT chelating agent and salt  
 PS Claim 5; Page 40; 57pp; English.  
 CC W02285 and W02286 are troponin I fragments used to exemplify the  
 CC usefulness of an aqueous composition (may be lyophilised) used as an  
 CC aqueous calibrator and control solution for diagnostic assays for  
 CC cardiac proteins and peptides. The stabilising solution comprises a  
 CC buffer, a reducing agent (e.g. 2-mercaptoethanol or N-acetyl-cysteine),  
 CC a stabilising protein (e.g. albumin or casein), a chelating agent (e.g.  
 CC EDTA or EGTA) a salt (e.g. NaCl), a blocking agent (especially gelatin)  
 CC and a bulking agent (e.g. trehalose, glucose, sucrose, galactose, etc.)  
 CC The composition is especially useful for diagnostic assays of  
 CC troponin, myoglobin, creatine kinase (CK), CK isoenzymes, lactate  
 CC dehydrogenase (LD), LD isoenzymes, myosin and fragments of these. The  
 CC composition may be used, e.g. in tests for acute myocardial infarction.  
 CC The stabilising composition is not derived from human serum, and thus  
 CC prevents exposure of the user (and manufacturing personnel) to many of

Query Match 34.2%; Score 233; DB 21; Length 35;  
 Best Local Similarity 100.0%; Pred. No. 7.62e-12;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 rayatephakhsksasrklqlklklllqakqel 35

QY 27 RAYATEPHAKHSKSISASRKLQLKLLQLLQIAKQEL 61

# RESULT 11

ID W37924 standard; peptide: 31 AA.  
 AC W37924;  
 DT 09-SEP-1998 (first entry)  
 DE N-terminal amino acid sequence of cardiac troponin I.  
 KW Cardiac troponin I; cTnI; acute myocardial infarction; inhibition;  
 KW Cardiac troponin I; cTnI; cardio-specific marker.  
 OS Homo sapiens.  
 PN WO9816255-A2.  
 PD 23-APR-1998.  
 PF 15-OCT-1997; U18368.  
 PR 15-OCT-1997; US-730111.  
 PR 15-OCT-1996; US-730111.  
 PA (NAV-) NAVIX INC.  
 PI Botyanszki J, Dave KI, Sintar E;  
 DR WPI: 98-251059/22.  
 PT Stabilising individual sub-units of multimeric protein by attaching  
 PT to polymer - particularly cardiac troponin sub-units for use as  
 PT controls in immunoassays for diagnosis of acute myocardial infarction  
 PS Disclosure; Page 14; 34pp; English.  
 CC This is the amino acid sequence of the N-terminal sequence of the  
 CC cardiac troponin I (cTnI) protein, acts as an inhibitory subunit to  
 CC cardiac troponin T (cTnT), which is released after an acute  
 CC myocardial infarction. The cTnI and cTnT are useful as  
 CC cardio-specific markers, particularly for early diagnosis of acute  
 CC myocardial infarction by immunoassays. The stabilised subunits are  
 CC used as control reagents in such assays.  
 SQ Sequence 31 AA;

Query Match 30.4%; Score 207; DB 32; Length 31;  
 Best Local Similarity 100.0%; Pred. No. 1.73e-09;  
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 madgssdaareppapapirrrssnyrayat 31

QY 1 MADGSSDAAREPPAPAPIRRRSSNYRAYAT 31

# RESULT 12

ID R55781 standard; peptide: 30 AA.  
 AC R55781;  
 DT 21-FEB-1995 (first entry)  
 DE Human cardiac troponin I N-terminal sequence.  
 KW Human cardiac troponin I; heart muscle necrosis; immunogen; epitope;  
 KW immunodiagnosis; acute myocardial infarction.  
 OS Homo sapiens.  
 PN DE4243648-A.  
 PD 07-JUL-1994.  
 PF 23-DEC-1992; 243648.  
 PR 23-DEC-1992; DE-243648.  
 PA (BOEF) BOEHRINGER MANNHEIM GMBH.  
 PI Borjya A, Donie F, Lill H, Seidel C;  
 DR WPI: 94-218764/27.  
 PT Rapid diagnosis of heart muscle necrosis in myocardial infarction  
 PT - by immunological test using new antibody recognising cardiac  
 PT troponin I N-terminal peptide  
 PS Claim 1; Page 8; 12pp; German.  
 CC The N-terminal 30 amino acids of human cardiac troponin I (R55781)  
 CC or subfragments of it (R55782-R55788) can be used as immunogens. The

CC antibodies raised by immunising animals (pref. sheep) with the  
CC peptides are useful for rapid diagnosis of heart muscle necrosis.  
SQ Sequence 30 AA;

Query Match 29.6%; Score 202; DB 11; Length 30;  
Best Local Similarity 100.0%; Pred. No. 4.88e-09;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 madgssdaareppapapirrsnyraya 30  
|||||  
Qy 1 MADGSSDAAREPPAPAPIRRSNYRAYA 30

## RESULT 13

ID W05041 standard; peptide; 31 AA.  
AC W05041;  
DT 12-JUN-1997 (first entry)  
DE N-terminus of cardiac troponin I.  
KW Cardiac troponin I; N-terminus; protease; inhibitor; cathepsin protease;  
KW cardiac tissue; serine protease; cysteine protease; aspartate protease;  
KW aminopeptidase protease; metalloendo-peptidase; myocardial infarction;  
KW human.  
OS Homo sapiens.  
PN US5560937-A.  
PD 01-OCT-1996.  
PF 24-AUG-1993; 110824.  
PR 24-AUG-1993; US-110824.  
PR 26-AUG-1994; US-296644.  
PA (SPEC-) SPECTRAL DIAGNOSTICS INC.  
PI Jackowski G, Lee L;  
DR WPI; 96-454492/45.  
PT Purifying human cardiac troponin I - by extn. of human cardiac  
PT tissue with a buffer contg. a protease inhibitor mixt. and affinity  
PT chromatography  
PS Claim 8; Column 13-14; 12pp; English.  
CC This sequence represents the N-terminus of human cardiac troponin I. The  
CC degradation of this sequence is inhibited by the protease inhibitor  
CC mixture used in the method of the invention. The method of the invention  
CC is for isolating a pure, stable cardiac troponin I preparation, where the  
CC troponin I has a molecular weight of about 28 kDa. The method comprises  
CC extracting human cardiac tissue with an aqueous extraction buffer at a pH  
CC of 7 to 9 which is 8 to 10 M in urea and contains a protease inhibitor  
CC mixture. The troponin I is then separated from the extract by affinity  
CC chromatography in the presence of the extraction buffer and calcium ions  
CC thereby to absorb the troponin I. The troponin I is then desorbed by  
CC washing with the aqueous extraction buffer containing EGTA. The protease  
CC inhibitor mixture used comprises at least two cathepsin protease  
CC inhibitors, at least one serine protease inhibitor and at least one  
CC cysteine protease inhibitor. The inhibitor mixture may also contain an  
CC aspartate protease inhibitor, an aminopeptidase protease inhibitor and  
CC a metalloendo-peptidase inhibitor. The isolated troponin I can be used as  
CC a standard in detection assays for early detection of myocardial  
CC infarction. The method provides pure and stable troponin which can  
CC provide for reproducible and reliable clinical testing.  
SQ Sequence 31 AA;

Query Match 29.6%; Score 202; DB 21; Length 31;  
Best Local Similarity 100.0%; Pred. No. 4.88e-09;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 adgssdaareppapapirrsnyrayate 31  
|||||  
Qy 2 ADGSSDAAREPPAPAPIRRSNYRAYATE 32

## RESULT 14

ID R73052 standard; peptide; 31 AA.  
AC R73052;  
DT 14-DEC-1995 (first entry)  
DE N-terminal sequence of cardiac troponin I.  
KW Cardiac troponin I; ctni; N-terminal region; cardiac specific;  
KW protease inhibitor; myocardial infarction.  
OS Homo sapiens.

PN CA2130280-A.  
PD 25-FEB-1995.  
PR 17-AUG-1994; 130280.  
PR 24-AUG-1993; US-110824.  
PA (SPEC-) SPECTRAL DIAGNOSTICS INC.  
PI Jackowski G, Lee L;  
DR WPI; 95-155575/21.  
PT New intact cardiac troponin I from heart tissue - isolated in  
PT presence of urea and protease inhibitors, useful as calibrator and  
PT quality control standard for troponin assay.  
PS Claim 8; Page 6; 30pp; English.  
CC The sequence shown is the N-terminal sequence of cardiac troponin I  
CC (ctni). This sequence was used in the development of a method for  
CC purifying cardiac troponin I with increased stability. The method was  
CC to extract the ctni in the presence of a mixture of protease inhibitors.  
CC This mixture of protease inhibitors includes at least 2 cathepsin  
CC protease inhibitors, at least 1 serine protease inhibitor and at least  
CC 1 cysteine protease inhibitor. This mixture is effective to inhibit  
CC degradation of the cardiac specific N-terminal region of ctni, which is  
CC this sequence. The advantage of this method is that it enables  
CC practically intact ctni that has good storage stability to be isolated.  
CC The ctni may then be used as a sensitive early indicator of myocardial  
CC infarction.  
SQ Sequence 31 AA;

Query Match 29.6%; Score 202; DB 14; Length 31;  
Best Local Similarity 100.0%; Pred. No. 4.88e-09;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 adgssdaareppapapirrsnyrayate 31  
|||||  
Qy 2 ADGSSDAAREPPAPAPIRRSNYRAYATE 32

## RESULT 15

ID W22598 standard; protein; 182 AA.  
AC W22598;  
DT 23-MAR-1998 (first entry)  
DE Human fast twitch skeletal muscle troponin I.  
KW Human; fast twitch skeletal muscle troponin; angiogenesis; inhibitor;  
KW tumour; ocular neovascularisation; arthritis; psoriasis;  
KW atherosclerotic plaque; nonunion fracture.  
OS Homo sapiens.  
PN W09730085-A1.  
PD 21-AUG-1997; U02439.  
PF 14-FEB-1997; US-602941.  
PR 16-FEB-1996; US-602941.  
PA (CHIL-) CHILDRENS MEDICAL CENT.  
PI Langer RS, Moses MA, Sytkowski A, Wiederschain DG,  
PI Wu I;  
DR WPI; 97-424977/39.  
PT Use of troponin subunits as angiogenesis inhibitors - used for  
PT treating e.g. tumours, ocular neovascularisation, arthritis,  
PT psoriasis, atherosclerotic plaques or nonunion fractures  
PS Claim 1; Page 9; 51pp; English.  
CC A novel pharmaceutical composition has been developed which comprises a  
CC carrier and an angiogenesis inhibiting amount of a peptide which is:  
CC (a) an inhibitor of basic fibroblast growth factor (bFGF)-stimulated  
CC bovine endothelial cell proliferation having an IC50 of at least  
CC 10 nM; (b) greater than 75 amino acids in length; and (c) greater  
CC than 80% homologous with a subunit selected from human fast-twitch  
CC troponin subunit C, subunit I or subunit T. The present sequence  
CC represents human fast-twitch troponin subunit I. The compositions can  
CC be used for inhibiting atopic angiogenesis. They can be used to treat a  
CC cancerous condition, or to prevent progression from a pre-neoplastic or  
CC non-malignant state into a neoplastic or a malignant state. They can  
CC also be used to treat ocular disorders associated with  
CC neovascularisation such as neovascular glaucoma, diabetic retinopathy,  
CC retinoblastoma, retrolental fibroplasia, uveitis, retinopathy of  
CC prematurity, macular degeneration, corneal graft neovascularisation as  
CC well as other eye inflammatory diseases, ocular tumour and diseases  
CC associated with choroidal or iris neovascularisation. They can also be  
CC used to treat other disorders e.g. haemangioma, arthritis, psoriasis,

CC angiofibroma, atherosclerotic plaques, delayed wound healing,  
CC granulations, haemophilic joints, hypertrophic scars, nonunion  
CC fractures, Osler-Weber syndrome, pyogenic granuloma, scleroderma,  
CC trachoma, and vascular adhesions.  
SQ Sequence 182 AA;  
Query Match 29.5%; Score 201; DB 26; Length 182;  
Best Local Similarity 39.7%; Pred. No. 5.99e-09;  
Matches 25; Conservative 21; Mismatches 16; Indels 1; Gaps 1;  
Db 6 knraitarrqhlksvmlqiaatelekeesrreaekqnylaehcpplhipg-smsevqel 64  
Qy 37 KKSKLSASRKQLKLTLLQIAKQELERAEERRGKGRALSTRCPLELAGLGFALQDL 96  
Db 65 ckq 67  
Qy 97 CRQ 99

Search completed: Fri Jan 21 14:31:17 2000  
Job time : 60 secs.

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W P S R E H  
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(TW)

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm  
Run on: Fri Jan 21 14:29:29 2000; MasPar time 6.59 Seconds  
Tabular output not generated. 602.084 Million cell updates/sec

Title: >US-09-176-546-2  
Description: (1-99) from US09176546.pap  
Perfect Score: 682  
Sequence: 1 MADGSSDAAREPRPAPR.....CQPLELAGLGAELQDLQCR 99

Scoring table: PAM 150  
Gap 11

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: p1r60  
1:p1r1 2:p1r2 3:p1r3 4:p1r4

Statistics: Mean 40.178; Variance 87.144; scale 0.461W

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	682	100.0	210	1	TPHUIC	troponin I, cardiac m
2	614	90.0	211	2	A53805	troponin I, cardiac -
3	610	89.4	211	2	A60124	troponin I, cardiac m
4	608	89.1	211	2	I56441	troponin I - rat
5	596	86.8	216	1	TPRBIC	troponin I, cardiac m
6	585	85.9	211	2	A29994	troponin I, cardiac m
7	431	63.2	208	2	A41030	troponin I, cardiac m
8	429	62.9	244	2	I51408	cardiac troponin I -
9	237	34.8	187	2	B44786	troponin I, slow skel
10	231	33.9	187	1	TPHUW	troponin I, slow skel
11	219	32.1	184	1	TPRBIW	troponin I, slow skel
12	210	30.8	142	2	JC5611	troponin I alpha - se
13	209	30.6	142	2	JC5612	troponin I beta - sea
14	208	30.5	182	1	TPRBI	troponin I, fast skel
15	205	30.1	182	2	A44786	troponin I, fast skel
16	201	29.5	182	1	TPHUIS	troponin I, fast skel
17	193	28.3	173	2	JC5610	troponin I - sea squi
18	192	28.2	183	2	A23569	troponin I, fast skel
19	192	28.2	183	1	TPRHIS	troponin I, fast skel
20	152	22.3	176	2	S70008	troponin I - Atlantic
21	144	21.1	208	2	A40547	troponin I - fruit fl
22	143	21.0	260	2	B38594	troponin I - fruit fl
23	136	19.9	201	2	A31484	troponin I, fast skel

24	123	18.0	208	2	A38594	troponin I - fruit fl	1.39e-04
25	105	15.4	292	2	JE0233	troponin-I - scallop	3.75e-02
26	101	14.8	258	2	I53021	troponin T - human	1.23e-01
27	101	14.8	886	2	S07132	hypothetical protein	1.23e-01
28	100	14.7	295	2	D56279	coxL 3'-region hypoth	1.64e-01
29	93	13.6	234	2	B44459	troponin T, fast skel	1.21e+00
30	93	13.6	249	2	A44459	troponin T, fast skel	1.21e+00
31	93	13.6	266	1	TPRBT	troponin T, fast skel	1.21e+00
32	92	13.5	272	2	A24824	troponin T, fast skel	1.60e+00
33	90	13.2	140	2	I38855	centromere protein-A	2.77e+00
34	90	13.2	314	2	JC4951	troponin T - scallop	2.77e+00
35	90	13.2	399	2	G71242	probable 26S proteina	2.77e+00
36	90	13.2	410	2	C69197	ATP-dependent 26S pro	2.77e+00
37	90	13.2	518	2	C70887	probable Propionyl-Co	2.77e+00
38	90	13.2	564	2	S73615	threonine--tRNA ligas	2.77e+00
39	90	13.2	1992	2	A47297	myosin heavy chain fo	2.77e+00
40	89	13.0	382	1	A44056	nucleocapsid protein	3.64e+00
41	89	13.0	484	2	JU0091	sucrose alpha-glucosi	3.64e+00
42	88	12.9	289	2	D71475	probable AMP nucleosi	4.77e+00
43	88	12.9	810	2	S67050	probable membrane pro	4.77e+00
44	87	12.8	593	2	A29607	phenylalanine amonia	6.24e+00
45	87	12.8	716	2	A56628	phenylalanine amonia	6.24e+00

ALIGNMENTS

RESULT 1

ENTRY TPHUIC #type complete  
TITLE troponin I, cardiac muscle - human  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 03-May-1994 #sequence\_revision 03-May-1996 #text\_change 05-Sep-1997

ACCESSIONS A61229; JN0837; S11522; A33185; S63690

REFERENCE A61229  
#authors Hunkeler, N.M.; Kullman, J.; Murphy, A.M.  
#journal Circ. Res. (1991) 69:1409-1414  
#title Troponin I isoform expression in human heart.  
#cross-references MUID:92035427  
#accession A61229  
#status not compared with conceptual translation

REFERENCE JN0837  
#molecule\_type mRNA  
#residues 1-210 #label HUN  
#authors Armour, K.L.; Harris, W.J.; Tempest, P.R.  
#journal Gene (1993) 131:287-292  
#title Cloning and expression in Escherichia coli of the cDNA encoding human cardiac troponin I.  
#cross-references MUID:94010323  
#accession JN0837

REFERENCE S11522  
#molecule\_type mRNA  
#residues 1-210 #label AR2  
#cross-references GB:M64247; NID:G339966; PID:G339967  
#authors Vallins, W.J.; Brand, N.J.; Dabhade, N.; Butler-Browne, G.; Yacoub, M.H.; Barton, P.J.R.  
#journal FEBS Lett. (1990) 270:57-61  
#title Molecular cloning of human cardiac troponin I using polymerase chain reaction.  
#cross-references MUID:91032031  
#accession S11522

REFERENCE S12886  
#molecule\_type mRNA  
#residues 1-85, T' 87-210 #label VAL  
#cross-references EMBL:X54163; NID:G37427; PID:G37428  
#authors Mittmann, K.; Jaquet, K.; Heilmeyer Jr., L.M.G.  
#journal FEBS Lett. (1990) 273:41-45  
#title A common motif of two adjacent phosphoserines in bovine, rabbit and human cardiac troponin I.  
#cross-references MUID:91032199  
#contents annotation; acetylated amino end; phosphorylation sites  
#gene GDB:TNNI3  
#cross-references GDB:125309; OMIM:191044

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#map_position 19p13.2-19q13.2
COMPLEX
troponin is a heterotrimer with one molecule each of troponin
C. (calcium binding component), troponin I (inhibitory
component), and troponin T (tropomyosin-binding component)

FUNCTION
#description binds actin and inhibits myosin ATPase activity; with
tropomyosin mediates contraction of vertebrate striated
muscle in response to calcium
#pathway muscle contraction
#superfamily troponin I
CLASSIFICATION #superfamily troponin I
KEYWORDS actylated amino end; actin binding; cardiac muscle; heart;
muscle contraction; phosphoprotein
FEATURE
2 #modified_site acetylated amino end (Ala) (in mature
form) #status experimental\
23,24 #binding_site phosphate (Ser) (covalent) (by
CAMP-dependent kinase) #status experimental
SUMMARY #length 210 #molecular-weight 24007 #checksum 1669

Query Match 100.0%; Score 682; DB 1; Length 210;
Best Local Similarity 100.0%; Pred. No. 1.31e-103;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MADSSDAAREPPAPAPIRRRSSNYRAYATEPHAKKSKISASRKLQTLMLQIAKQ 60
QY 1 MADSSDAAREPPAPAPIRRRSSNYRAYATEPHAKKSKISASRKLQTLMLQIAKQ 60
Db 61 LERAEERREKGRALSTRCQPLELAGLGFALQDLQCRQ 99
QY 61 LERAEERREKGRALSTRCQPLELAGLGFALQDLQCRQ 99

RESULT 2
ENTRY #type complete
TITLE troponin I, cardiac - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change
17-Mar-1999
ACCESSION A53805; A53108
REFERENCE Guo, X.; Wattanapornpool, J.; Palmiter, K.A.; Murphy, A.M.;
Solaro, R.J.
#journal J. Biol. Chem. (1994) 269:15210-15216
#title Mutagenesis of cardiac troponin I. Role of the unique
NH-2-terminal peptide in myofilament activation.
#cross-references MUID:94253083
#accession A53805
#status preliminary
#molecule_type mRNA
#residues 1-211 #label GUO
#cross-references GB:009181; NID:9484093; PID:g508866
REFERENCE A53108
#authors Ausoni, S.; Campione, M.; Picard, A.; Moretti, P.; Vitadello,
M.; De Nardi, C.; Schiaffino, S.
#journal J. Biol. Chem. (1994) 269:339-346
#title Structure and regulation of the mouse cardiac troponin I
gene.
#cross-references MUID:94103233
#accession A53108
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-211 #label RES
#cross-references EMBL:222784; NID:g313104; PID:g313105
GENETICS
#introns 4/2; 8/3; 37/3; 51/3; 95/3; 125/3; 184/3
CLASSIFICATION #superfamily troponin I
KEYWORDS actin binding; heart; phosphoprotein
SUMMARY #length 211 #molecular-weight 24259 #checksum 7181

Query Match 90.0%; Score 614; DB 2; Length 211;
Best Local Similarity 89.0%; Pred. No. 8.63e-91;
Matches 89; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

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Db 1 MADSSDAAGFPQAPAPVRRSSNYRAYATEPHAKKSKISASRKLQTLMLQIAKQ 60
QY 1 MADSSDAAREPPAPAPIRRRSS-NYRAYATEPHAKKSKISASRKLQTLMLQIAKQ 59
Db 61 EMERAEERREKGRVLTTRCQPLELDGLGFELQDLQCRQ 100
QY 60 ELERAEERREKGRALSTRCQPLELAGLGFALQDLQCRQ 99

RESULT 3
ENTRY #type complete
TITLE troponin I, cardiac muscle - rat
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change
31-Oct-1997
ACCESSION A60124; A38398; S14849
REFERENCE A60124
#authors Ausoni, S.; De Nardi, C.; Moretti, P.; Gorza, L.; Schiaffino,
S.
#journal Development (1991) 112:1041-1051
#title Developmental expression of rat cardiac troponin I mRNA.
#accession A60124
#molecule_type mRNA
#residues 1-211 #label AUS
#cross-references EMBL:X58499; NID:g56022; PID:g56023
REFERENCE A38398
#authors Murphy, A.M.; Jones II, L.; Sims, H.F.; Strauss, A.W.
#journal Biochemistry (1991) 30:707-712
#title Molecular cloning of rat cardiac troponin I and analysis of
troponin I isoform expression in developing rat heart.
#cross-references MUID:91105162
#accession A38398
#molecule_type mRNA
#residues 1-211 #label MUR
#cross-references GB:M57679; GB:J05304; NID:g207509; PID:g207510
CLASSIFICATION #superfamily troponin I
KEYWORDS actin binding; cardiac muscle; heart
SUMMARY #length 211 #molecular-weight 24159 #checksum 7678

Query Match 89.4%; Score 610; DB 2; Length 211;
Best Local Similarity 89.0%; Pred. No. 4.87e-90;
Matches 89; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

Db 1 MADSSDAAGFPQAPAPVRRSSNYRAYATEPHAKKSKISASRKLQTLMLQIAKQ 60
QY 1 MADSSDAAREPPAPAPIRRRSS-NYRAYATEPHAKKSKISASRKLQTLMLQIAKQ 59
Db 61 EMERAEERREKGRVLTTRCQPLELDGLGFELQDLQCRQ 100
QY 60 ELERAEERREKGRALSTRCQPLELAGLGFALQDLQCRQ 99

RESULT 4
ENTRY #type complete
TITLE troponin I - rat
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
23-Feb-1997
ACCESSION I56441
REFERENCE I56441
#authors Martin, A.F.; Orłowski, J.
#journal J. Mol. Cell. Cardiol. (1991) 23:583-588
#title Molecular cloning and developmental expression of the rat
cardiac-specific isoform of troponin I.
#cross-references MUID:91359315
#accession I56441
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-211 #label RES
#cross-references GB:M92074; NID:g207515; PID:g207516
CLASSIFICATION #superfamily troponin I
SUMMARY #length 211 #molecular-weight 24163 #checksum 7943

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#journal J. Biol. Chem. (1991) 266:19659-19665
#title Structure and developmental expression of troponin I isoforms. cDNA clone analysis of avian cardiac troponin I mRNA.
#cross-references MUID:92011768
#accession A41030
#molecule_type mRNA
#residues 1-208 #label HAS
#cross-references GB:M73702; NID:g213647; PID:g213648
CLASSIFICATION #superfamily troponin I
KEYWORDS actin binding; cardiac muscle; heart
SUMMARY #length 208 #molecular-weight 23601 #checksum 578

Query Match 63.2%; Score 431; DB 2; Length 208;
Best Local Similarity 67.4%; Pred. No. 7,90e-57;
Matches 62; Conservative 12; Mismatches 17; Indels 1; Gaps 1;

Db 2 ABEPPKPPRRSSANYRYPVPHAKRQKISASRKLQKTLTLLQAKRDLERQEE 61
QY 9 AREPRPAPIRRRSS-NRYAYATEPHAKKKSISASRKLQKTLTLLQAKQLERAE 67
Db 62 RAGEKQRHGELCPPELDGLGVAQLQELCRE 93
QY 68 RRGKGRALSTRCPQLEAGLGLFAELQDLCRQ 99

RESULT 8
ENTRY I51408 #type complete
TITLE cardiac troponin I - African clawed frog
ORGANISM #formal_name Xenopus laevis #common_name African clawed frog
DATE 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Feb-1997
ACCESSIONS I51408
REFERENCE I51408
#authors Drysdale, T.A.; Tonissen, K.F.; Patterson, K.D.; Crawford, M.J.; Krieg, P.A.
#journal Dev. Biol. (1994) 165:432-441
#title Cardiac troponin I is a heart-specific marker in the Xenopus embryo: expression during abnormal heart morphogenesis.
#cross-references MUID:95046865
#accession I51408
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-244 #label DRY
#cross-references GB:L25721; NID:g410050; PID:g410051
CLASSIFICATION #superfamily troponin I
KEYWORDS heart
SUMMARY #length 244 #molecular-weight 28198 #checksum 1120

Query Match 62.9%; Score 429; DB 2; Length 244;
Best Local Similarity 60.0%; Pred. No. 1.83e-56;
Matches 60; Conservative 23; Mismatches 16; Indels 1; Gaps 1;

Db 25 VAEPPKPPAPPPPLIRRRSSANYRYPVPHAKRQKISASRKLQNTMMLQIAKA 84
QY 1 MADGSDAAREPAPAPIRRRSS-NRYAYATEPHAKKKSISASRKLQKTLTLLQIAK 59
Db 85 EMEREERAREKRYLAERQPLQLSLGRSELODLQCE 124
QY 60 ELERAEERGERGRALSTRCPQLEAGLGLFAELQDLCRQ 99

RESULT 9
ENTRY B44786 #type complete
TITLE troponin I, slow skeletal muscle - rat
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 19-Mar-1993 #sequence_revision 19-Mar-1993 #text_change 17-Mar-1999
ACCESSIONS B44786
REFERENCE A44786
#authors Koppe, R.I.; Hallauer, P.L.; Karpatti, G.; Hastings, K.E.M.
#journal J. Biol. Chem. (1989) 264:14327-14333
#title cDNA clone and expression analysis of rodent fast and slow

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#cross-references MUID:89340548
#accession B44786
#status preliminary
#molecule_type mRNA
#residues 1-187 #label KOP
#cross-references GB:J04993; NID:g207517; PID:g207518
CLASSIFICATION #superfamily troponin I
KEYWORDS skeletal muscle
SUMMARY #length 187 #molecular-weight 21724 #checksum 7736

Query Match 34.8%; Score 237; DB 2; Length 187;
Best Local Similarity 53.7%; Pred. No. 1.68e-22;
Matches 36; Conservative 12; Mismatches 19; Indels 0; Gaps 0;

Db 2 PEVERKSKITASRKLMLKSLAKAKCEWQEEERAEKRVYLSERIPTLOTQRLSLA 61
QY 33 PHAKKSKISASRKLQKTLTLLQAKQLERAEERGERGRALSTRCPQLEAGLGLFAE 92
Db 62 LQDLCRE 68
QY 93 LQDLCRQ 99

RESULT 10
ENTRY TPHUIW #type complete
TITLE troponin I, slow skeletal muscle - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 06-Jan-1995 #sequence_revision 03-May-1996 #text_change 18-Sep-1998
ACCESSIONS A53740; A53555
REFERENCE A53740
#authors Corin, S.J.; Juhasz, O.; Zhu, L.; Conley, P.; Kedes, L.; Wade, R.
#journal J. Biol. Chem. (1994) 269:10651-10659
#title Structure and expression of the human slow twitch skeletal muscle troponin I gene.
#cross-references MUID:94193765
#accession A53740
#molecule_type DNA
#residues 1-187 #label COR
#cross-references GB:L21905
#authors Wade, R.; Eddy, R.; Shows, T.B.; Kedes, L.
#journal Genomics (1990) 7:346-357
#title cDNA sequence, tissue-specific expression, and chromosomal mapping of the human slow-twitch skeletal muscle isoform of troponin I.
#cross-references MUID:90307007
#accession A53555
#molecule_type mRNA
#residues 1-181, NA, 184-187 #label WAD
#cross-references GB:J04760; NID:g339964; PID:g339965
GENETICS
#gene GDB:TNNI1
#map_position lq32-lq32
#introns 4/2; 5/3; 19/3; 63/3; 93/3; 152/3
#note the first intron occurs before the initiator codon
#complex troponin I is a heterotrimer with one molecule each of troponin C (calcium binding component), troponin I (inhibitory component), and troponin T (tropomyosin-binding component)

FUNCTION
#description binds actin and inhibits myosin ATPase activity; with tropomyosin mediates contraction of vertebrate striated muscle in response to calcium
#pathway muscle contraction
#classification #superfamily troponin I
#keywords acetylated amino end; actin binding; muscle contraction; skeletal muscle
#feature
2 #modified site acetylated amino end (Pro) (in mature form) #status predicted

```

```
SUMMARY      #length 187   #molecular-weight 21692   #checksum 7017

Query Match          33.9%; Score 231; DB 1; Length 187;
Best Local Similarity 50.7%; Pred. No. 1.72e-21;
Matches              34; Conservative 14; Mismatches 19; Indels 0; Gaps 0;

Db    2 PEVERPKPTASKRLLKSLMLAKAKECWGEHREAREAEKVRYLAERIPALOTRGLSA 61
     I :|||:||||| ||:: |:: |||| ::|| |:: |:: |:: |:: |:: |: 
QY    33 PHAKKSISASRKQLKLTLIIQAQELEAREERGEKGRAUSTRCQPDLAGLGFEE 92
     Db        62 LQDLCRR 68               ||||||:
     QY       93 LQDLCRR 99             ||||||:

RESULT 11
ENTRY  TPRIW         #type complete
TITLE troponin I, slow skeletal muscle - rabbit
ORGANISM #formal_name Oryctolagus cuniculus #common_name domestic
DATE 30-Apr-1979 #sequence_revision 30-Apr-1979 #text_change
REFERENCE A03089
AUTHORS Grand, R.J.A.; Wilkinson, J.M.
JOURNAL Biochem. J. (1977) 167:183-192
TITLE The amino acid sequence of rabbit slow-muscle troponin I.
#cross-references MUID:78060292
ACCESSION A03089
#molecule_type protein
#residues 1-184 #label GRA
#note troponin is a heterotrimer with one molecule each of tropomyosin C (calcium binding component), troponin I (inhibitory component), and troponin T (tropomyosin-binding component)

FUNCTION
description binds actin and inhibits myosin ATPase activity; with tropomyosin mediates contraction of vertebrate striated muscle in response to calcium
pathway muscle contraction
CLASSIFICATION #superfamily troponin I
KEYWORDS actin binding
FEATURE 1
SUMMARY #modified_site blocked amino end (Pro) (partial) (probably acetylated) #status experimental
#length 184 #molecular-weight 21143 #checksum 4497

Query Match          32.1%; Score 219; DB 1; Length 184;
Best Local Similarity 52.2%; Pred. No. 1.72e-19;
Matches              35; Conservative 13; Mismatches 17; Indels 2; Gaps 2;

Db    1 PEVERSKITASKRL-LKSLMLAAKA-ECPQHARAEAEKVRYLAERIPALOTRGLSA 58
     I :||||:||||| ||:: |:: ||:: |:: ||:: |:: |:: |:: |:: |: 
QY    33 PHAKKSISASRKQLKLTLIIQAQELEAREERGEKGRAUSTRCQPDLAGLGFEE 92
     Db        59 LQDLCRR 65               |||||||
     QY       93 LQDLCRR 99             |||||||

RESULT 12
ENTRY JC5611           #type complete
TITLE troponin I alpha - sea squirt (Halocynthia roretzi)
ORGANISM #formal_name Halocynthia roretzi
DATE 23-Sep-1997 #sequence_revision 17-Oct-1997 #text_change
REFERENCE JC5611
AUTHORS Yuasa, H.J.; Sato, S.; Yamamoto, H.; Takagi, T.
JOURNAL J. Biochem. (1997) 122:374-380
TITLE Primary structure of troponin I isoforms from the ascidian Halocynthia roretzi.
#cross-references MUID:98021076
```

```

##cross-references GB:L04347
##experimental_source skeletal muscle
##note
sequence extracted from NCBI backbone (NCBIP:120236) and
corrected to correspond with the published sequence
the authors translated the codons GGC for residue 56 as
Gln, and TAT for residue 80 as Thr

REFERENCE
A93193
#authors
Wilkinson, J.M.; Grand, R.J.A.
#journal
Nature (1978) 271:31-35
#title
Comparison of amino acid sequence of troponin I from
different striated muscles.
#cross-references MUID:78114026
#accession
A93193
#molecule_type protein
#residues 2-154,158-182 #label WIL

REFERENCE
A90286
#authors
Wilkinson, J.M.; Grand, R.J.A.
#journal
Biochem. J. (1975) 149:493-496
#title
The amino acid sequence of troponin I from rabbit skeletal
muscle.
#cross-references MUID:76039510
#accession
A90286
#molecule_type protein
#residues 2-114,'R',115-154,158-182 #label W12

REFERENCE
A91408
#authors
Moir, A.J.G.; Wilkinson, J.M.; Perry, S.V.
#journal
FEBS Lett. (1974) 42:253-256
#title
The phosphorylation sites of troponin I from white skeletal
muscle of the rabbit.
#cross-references MUID:74309023
#contents
annotation; phosphorylation sites

REFERENCE
A91407
#authors
Huang, T.S.; Bylund, D.B.; Stull, J.T.; Krebs, E.G.
#journal
FEBS Lett. (1974) 42:249-252
#title
The amino acid sequences of the phosphorylated sites in
troponin-I from rabbit skeletal muscle.
#cross-references MUID:74308154
#contents
annotation; phosphorylation sites

REFERENCE
I46471
#authors
Putney, S.D.; Herlihy, W.C.; Schimmel, P.
#journal
Nature (1983) 302:718-721
#title
A new troponin T and cDNA clones for 13 different muscle
proteins, found by shotgun sequencing.
#cross-references MUID:83167564
#accession
I46514
#status
preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 166-178 #label PUT

COMPLEX
##cross-references EMBL:V00898; NID:g1738; PID:g929767
troponin is a heterotrimer with one molecule each of troponin
C (calcium binding component), troponin I (inhibitory
component), and troponin T (tropomyosin-binding component)

FUNCTION
#description
binds actin and inhibits myosin ATPase activity; with
tropomyosin mediates contraction of vertebrate striated
muscle in response to calcium

#pathway
muscle contraction

CLASSIFICATION
#superfamily troponin I
KEYWORDS
acetylated amino end; actin binding; muscle contraction;
phosphoprotein; skeletal muscle

FEATURE
2
#modified site acetylated amino end (Gly) (in mature
form) #status experimental\
12
#binding_site phosphate (Thr) (covalent) (by
CAMP-dependent kinase) #status experimental\
20,90,118
#binding_site phosphate (Ser) (covalent) (by
CAMP-dependent kinase) #status experimental
SUMMARY
#length 182 #molecular-weight 21214 #checksum 8861

Query Match 30.5%; Score 208; DB 1; Length 182;
Best Local Similarity 42.9%; Pred. NO. 1.12e-17;
Matches 27; Conservative 19; Mismatches 16; Indels 1; Gaps 1;

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```

Db 6 KNRRAITARRQHLKSVMLQIAATELEKEBGRRAEKQNYLAECPPPLSLPG-SMAEVOEL 64
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 37 KKSISASRKQLKTLILLQIAQELEREAEERGERGKRALSTRCPQLELAGLGFALQDL 96
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 65 CKQ 67
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 97 CRQ 99

RESULT 15
ENTRY A44786 #type complete
TITLE troponin I, fast skeletal muscle - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 19-Mar-1993 #sequence_revision 19-Mar-1993 #text_change
17-Mar-1999

ACCESSIONS A44786
REFERENCE A44786
#authors Koppe, R.I.; Hallauer, P.L.; Karpatti, G.; Hastings, K.E.M.
#journal J. Biol. Chem. (1989) 264:14327-14333
#title cDNA clone and expression analysis of rodent fast and slow
skeletal muscle troponin I mRNAs.
#cross-references MUID:89340548
#accession A44786
#status preliminary
#molecule_type mRNA
#residues 1-182 #label KOP
#cross-references GB:J04952; NID:g202164; PID:g202165
CLASSIFICATION #superfamily troponin I
KEYWORDS skeletal muscle
SUMMARY #length 182 #molecular-weight 21357 #checksum 306

Query Match 30.1%; Score 205; DB 2; Length 182;
Best Local Similarity 41.3%; Pred. No. 3.49e-17;
Matches 26; Conservative 20; Mismatches 16; Indels 1; Gaps 1;

Db 6 KNRRAITARRQHLKSVMLQIAATELEKEBGRRAEKQNYLAECPPPLSLPG-SMAEVOEL 64
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 37 KKSISASRKQLKTLILLQIAQELEREAEERGERGKRALSTRCPQLELAGLGFALQDL 96
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 65 CKQ 67
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 97 CRQ 99

Search completed: Fri Jan 21 14:29:58 2000
Job time : 29 secs.

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Result No.	Query		Length	DB	ID	Description	Pred. No.
	Score	Match					
1	252	37.0	188	13	Q90350	TROPONIN I SLOW SKELET	4.478-27
2	210	30.8	142	5	O01355	LARVAL TROPONIN I BETA	1.548-19
3	209	30.6	142	5	O01356	LARVAL TROPONIN I BETA	2.318-19
4	193	28.3	173	5	O01354	TROPONIN I.	1.438-16
5	180	26.4	229	5	O77010	TROPONIN I.	2.438-14
6	163	23.9	176	13	Q90365	TROPONIN-I.	1.738-11
7	161	23.6	172	13	O13095	TROPONIN-I ISOFORM 3.	3.718-11
8	160	23.5	180	13	O13094	TROPONIN-I ISOFORM 2.	5.428-11
9	152	22.3	176	13	Q90366	TROPONIN-I.	1.108-09
10	117	17.2	172	13	O13093	FAST MYOTOMAL MUSCLE T	2.998-04
11	106	15.5	817	4	O75420	ORE2.	1.148-02
12	105	15.4	271	5	O44077	TROPONIN I (FRAGMENT).	1.588-02
13	104	15.2	293	5	O15988	TROPONIN I.	2.188-02
14	104	15.2	314	5	O15987	TROPONIN I.	2.188-02
15	101	14.8	306	5	Q23585	SIMILAR TO TROPONIN I.	5.658-02
16	101	14.8	885	2	Q53031	ATP OPERON (FRAGMENT).	5.658-02
17	100	14.7	295	2	O1326	COXMSL GENE CLUSTER.	7.738-02
18	98	14.4	1422	5	O00914	PFSNF21.	1.448-01
19	97	14.2	197	5	O44572	W03F8.1 PROTEIN.	1.978-01
20	97	14.2	574	4	O75134	K1AA0639 PROTEIN (FRAG	1.978-01

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Query Match      28.3%; Score 193; DB 5; Length 173;
Best Local Similarity 44.8%; Pred.No.1.43e-16;
Matches          25; Conservative 16; Mismatches 14; Indels 1; Gaps 1;

Db    5 RKONLSMLNKAREDKLEAEVKADEKKKIILNSRIEPLSNLGGMSEQDLKDLCRE 60
     QY   |||::|| :::::|| |::: || :|::|| ::::: -||||:
         45 RKLQLTKLLQTAKQELEREAERGEGKRALSTRCOPL-ELAGLGFAELQDLCRQ 99

RESULT        5
ID            077010 PRELIMINARY; PRT; 229 AA.
AC            077010;
DT            01-NOV-1998 (TREMBLREL. 08, CREATED)
DT            01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT            01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE            TROPONIN I.
OS            CIONA INTESTINALIS.
OC            EUKARYOTA; METAZOA; CHORDATA; UROCHORDATA; ASCIDIACEA; PHLEBOBRANCHIA;
OC            CLONIDAE; CIONA.
RN            [1]
RP            SEQUENCE FROM N.A.
RC            TISSUE=HEART;
RX            MEDLINE; 98070375.
RA            MACLEAN D.W., MEDEL T.H., HASTINGS K.E.;
RT            "Tissue-specific alternative splicing of ascidian troponin I
RT            isoforms. Redesign of a protein isoform-generating mechanism during
RT            chordate evolution.";
RL            J. BIOL. CHEM. 272:32115-32120(1997).
DR            EMBL; U94693; G335039; -.
SQ            SEQUENCE 229 AA; 26347 MW; 36E73D53 CRC32;

Query Match      26.4%; Score 180; DB 5; Length 229;
Best Local Similarity 41.0%; Pred.No. 2.43e-14;
Matches          25; Conservative 15; Mismatches 20; Indels 1; Gaps 1;

Db    56 KMTHQRKMMLKSMLNKRAREDKREMEQAEEAKKAEIORSLEPGLSNGMSSELMDLCR 115
     QY   ||: ||::|| :::::|| :::: |||::|| :::: |||::|| :::: |||::||
         40 KISASRKQLQKTLLLTQAKQELESREAERGEKGALSTRCPGLE-LAGLGFAELQDLCR 98

Db    116 E 116
     QY   ;

RESULT        6
ID            Q90365 PRELIMINARY; PRT; 176 AA.
AC            Q90365;
DT            01-NOV-1996 (TREMBLREL. 01, CREATED)
DT            01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT            01-NOV-1996 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE            TROPONIN-I
OS            CLUPEA HARENUS (ATLANTIC HERRING).
OC            EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
OC            TELEOSTEI; CLUPEOMORPHA; CLUPEIDAE; CLUPEINAE; CLUPEA.
RN            [1]
RP            SEQUENCE FROM N.A.
RC            STRAIN=CLYDE-STOCK (BUCHAN BANK); TISSUE-WHOLE ORGANISM;
RA            HOOGSON P.A., LEAVAR M.J., GEORGE S.G.;
RL            SUBMITTED (JAN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR            EMBL; U20111; G643662; -.
DR            PFAM; PF00992; Troponin; 1.
SQ            SEQUENCE 176 AA; 19641 MW; E2E04DAB CRC32;

Query Match      23.9%; Score 163; DB 13; Length 176;
Best Local Similarity 36.7%; Pred.No. 1.73e-11;
Matches          22; Conservative 19; Mismatches 18; Indels 1; Gaps 1;

Db    5 KWTSRRKHHLKSVMLATAATRLEOEADAATAAKEETYLDNCPSLDYPSS-SIEDLQKLCKE 63
     QY   ||::||| ::||::|| ||::|| |::: || |::: |||::|| :::: |||::||
         40 KISASRKQLQKTLLLTQAKQELESREAERGEKGALSTRCPGLELAGLGFAELQDLCRQ 99
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[illegible]

```

Qy      8 AARPRAPAPIRRSSNYRAYATEPHAKK-KSKISAS-RKLQLKTLL-LQI-AKOELER 63

Db      570 QPP-PR-EPARAQPN-HRVOLGGLGTAPLNQ 598
       : | | | | : | | | | : | | | | :
Qy      64 EAEERRGEKGALSTRCQPLEAGLGFAELQD 95
       : | | | | : | | | | : | | | | :

RESULT 12
ID      ID O44077 PRELIMINARY; PRT; 271 AA.
AC      AC O44077;
DT      DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
DT      DT 01-JUN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DE      DE TROPONIN I (FRAGMENT).
DE      DE TROPONIN I (FRAGMENT).
OS      OS CHLAMYS NIPONENSIS AKAZARA (AKAZARA SCALLOP) (JAPANESE SCALLOP).
OC      OC UKARIYOTA; METAZOA; MOLLUSCA; BIVALVIA; PTერიOMORPHIA; OSTREOIDA;
CC      CC PECTINIDAE; CHLAMYDS.
RN      RN [1]
RP      RP SEQUENCE FROM N.A.
RA      RA NISHITA K., OJIMA T., SOEJIMA T.;
RL      RL SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR      DR ENBL; AB009368; D1024680; -.
FT      FT NON_TER 1
SQ      SQ SEQUENCE 271 AA; 32068 MW; C9E22FB9 CRC32;

Query Match 15.4%; Score 105; DB 5; Length 271;
Best Local Similarity 28.8%; Pred. No. 1.58e-02;
Matches 17; Conservative 14; Mismatches 28; Indels 0; Gaps 0;

Db      123 LSPEKKMKLKLMQAAEDLANEAKAKAEKEKYINDLVKFSTDGKDVAALQALCKD 181
       : | | | | | | | | : | | | | : | | | | :
Qy      41 ISARKLQLKTLLLIQAQLEEREAEERRGEKGALSTRCQPLEAGLGFAELQDLCRQ 99
       : | | | | | | | | : | | | | : | | | | :

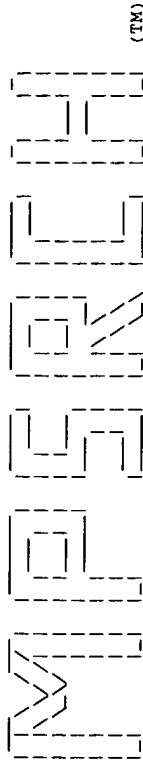
RESULT 13
ID      ID O15988 PRELIMINARY; PRT; 293 AA.
AC      AC O15988;
DT      DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT      DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DE      DE TROPONIN I.
DE      DE TROPONIN I.
OS      OS PATINOPECTEN YESSOENSIS (EZO GIANT SCALLOP) (YESSO SCALLOP).
OC      OC UKARIYOTA; METAZOA; MOLLUSCA; BIVALVIA; PTერიOMORPHIA; OSTREOIDA;
CC      CC PECTINIDAE; PATINOPECTEN.
RN      RN [1]
RP      RP SEQUENCE FROM N.A.
RA      RA HOTTA A.L.;
RL      RL SUBMITTED (OCT-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR      DR ENBL; AB008006; D1023723; -.
FT      FT PFAM; PF00992; Troponin; 1.
SQ      SQ SEQUENCE 293 AA; 34670 MW; 49299FDE CRC32;

Query Match 15.2%; Score 104; DB 5; Length 293;
Best Local Similarity 28.8%; Pred. No. 2.18e-02;
Matches 17; Conservative 14; Mismatches 28; Indels 0; Gaps 0;

Db      145 LSPEKKMKLKLMQAAEDLKNEAKAKAEKEKYINDLVKFSTDGKDVAALQALCKD 203
       : | | | | | | | | : | | | | : | | | | :
Qy      41 ISARKLQLKTLLLIQAQLEEREAEERRGEKGALSTRCQPLEAGLGFAELQDLCRQ 99
       : | | | | | | | | : | | | | : | | | | :

RESULT 14
ID      ID O15987 PRELIMINARY; PRT; 314 AA.
AC      AC O15987;
DT      DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT      DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DE      DE TROPONIN I.
DE      DE TROPONIN I.
OS      OS PATINOPECTEN YESSOENSIS (EZO GIANT SCALLOP) (YESSO SCALLOP).
OC      OC UKARIYOTA; METAZOA; MOLLUSCA; BIVALVIA; PTერიOMORPHIA; OSTREOIDA;
CC      CC PECTINIDAE; PATINOPECTEN.
RN      RN [1]
RP      RP SEQUENCE FROM N.A.
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm  
Run On: Fri Jan 21 14:27:43 2000; MasPar time 4.57 Seconds  
Tabular output not generated. 612.656 Million cell updates/sec

Title: >US-09-176-546-2  
Description: (1-99) from US09176546.ppep  
Perfect Score: 682  
Sequence: 1 MADGSSDAAREPRPAPR.....CQPLELAGLFAELQDLCRQ 99

Scoring table: PAM 150  
Gap 11

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: swiss-prot37  
1:swissprot

Statistics: Mean 41.275; Variance 77.899; scale 0.530

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	671	98.4	209	1	TRIC_HUMAN	TROPONIN I, CARDIAC MU 1.63e-116
2	603	88.4	210	1	TRIC_MOUSE	TROPONIN I, CARDIAC MU 7.86e-102
3	599	87.8	210	1	TRIC_RAT	TROPONIN I, CARDIAC MU 5.70e-101
4	586	85.9	211	1	TRIC_BOVIN	TROPONIN I, CARDIAC MU 3.54e-98
5	539	79.0	206	1	TRIC_RABIT	TROPONIN I, CARDIAC MU 4.07e-88
6	431	63.2	207	1	TRIC_COTJA	TROPONIN I, CARDIAC MU 2.78e-65
7	429	62.9	243	1	TRIC_XENLA	TROPONIN I, CARDIAC MU 7.28e-65
8	258	39.3	168	1	TRIC_CHICK	TROPONIN I, CARDIAC MU 4.71e-32
9	237	34.8	186	1	TRIS_RAT	TROPONIN I, SLOW SKELE 5.03e-26
10	231	33.9	186	1	TRIS_HUMAN	TROPONIN I, SLOW SKELE 7.12e-25
11	219	32.1	184	1	TRIS_RABIT	TROPONIN I, SLOW SKELE 1.36e-22
12	208	30.5	181	1	TRIF_RABIT	TROPONIN I, FAST SKELE 1.60e-20
13	205	30.1	181	1	TRIF_MOUSE	TROPONIN I, FAST SKELE 5.81e-20
14	203	29.8	181	1	TRIF_RAT	TROPONIN I, FAST SKELE 1.37e-19
15	201	29.5	181	1	TRIF_HUMAN	TROPONIN I, FAST SKELE 3.22e-19
16	192	28.2	182	1	TRIF_CHICK	TROPONIN I, FAST SKELE 1.48e-17
17	143	21.0	259	1	TRI_DROME	TROPONIN I, (TNI) (WING 6.49e-09
18	136	19.9	201	1	TRI_PONLE	TROPONIN I, 9.47e-08
19	110	16.1	564	1	FMRI_XENLA	FRAGILE X MENTAL RETAR 1.20e-03
20	103	15.1	548	1	FXRI_XENLA	FRAGILE X MENTAL RETAR 1.28e-02
21	101	14.8	257	1	TRT3_HUMAN	TROPONIN T, FAST SKELE 2.49e-02
22	93	13.6	278	1	TRT3_RABIT	TROPONIN T, FAST SKELE 3.24e-01
23	93	13.6	886	1	CHS_SAPMO	CHITIN SYNTHASE (EC 2. 3.24e-01

24	92	13.5	258	1	TRT3_RAT	TROPONIN T, FAST SKELE 4.43e-01
25	90	13.2	140	1	CENA_HUMAN	CENTROMERE PROTEIN A ( 8.19e-01
26	90	13.2	410	1	PRSI_METH	PUTATIVE 26S PROTEASE 8.19e-01
27	90	13.2	564	1	SYT_MYCPN	THREONYL-TRNA SYNTHETA 8.19e-01
28	89	13.0	382	1	NCAP_CVCAE	NUCLEOCAPSID PROTEIN. 1.11e+00
29	89	13.0	484	1	SCRE_VIBAL	SUCROSE-6-PHOSPHATE HY 1.11e+00
30	87	12.8	135	1	ZNTR_HAEIN	ZN(II)-RESPONSIVE REGU 2.03e+00
31	87	12.8	716	1	PALY_RHOTO	PHENYLALANINE AMMONIA- 2.03e+00
32	86	12.6	245	1	Y01A_MYCTU	HYPOTHETICAL 26.9 KD P 2.73e+00
33	86	12.6	294	1	HK5A_CHICK	HOMEOBOX PROTEIN NKX-2 2.73e+00
34	86	12.6	328	1	SGS3_DROER	SALIVARY GLUE PROTEIN 2.73e+00
35	86	12.6	468	1	BMP3_RAT	BONE MORPHOGENETIC PRO 2.73e+00
36	85	12.5	189	1	RL14_TRYBB	PROBABLE 40S RIBOSOMAL 3.66e+00
37	85	12.5	350	1	RS40_ARATH	ARGININE/SERINE-RICH S 3.66e+00
38	85	12.5	452	1	Y0A9_MYCTU	HYPOTHETICAL 47.5 KD P 3.66e+00
39	85	12.5	587	1	UL84_HCMVT	55 KD EARLY NONSTRUCTU 3.66e+00
40	85	12.5	614	1	FMR1_MOUSE	FRAGILE X MENTAL RETAR 3.66e+00
41	85	12.5	632	1	FMRI_HUMAN	FRAGILE X MENTAL RETAR 3.66e+00
42	85	12.5	797	1	PAT1_YEAST	TOPOISOMERASE II-ASSOC 3.66e+00
43	84	12.3	282	1	YHPQ_YEAST	HYPOTHETICAL 32.1 KD P 4.91e+00
44	84	12.3	400	1	NIFV_ENTAG	HOMOCITRATE SYNTHASE ( 4.91e+00
45	84	12.3	614	1	RUI7_HUMAN	U1 SMALL NUCLEAR RIBON 4.91e+00

ALIGNMENTS

RESULT 1	TRIC_HUMAN	STANDARD;	PRT;	209 AA.
AC	P19429;			
DT	01-FEB-1991 (REL. 17, CREATED)			
DT	01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)			
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)			
DE	TROPONIN I, CARDIAC MUSCLE.			
GN	TNNI3 OR TNNC1.			
OS	HOMO SAPIENS (HUMAN).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;			
OC	PRIMATES; CATARRHINI; HOMINIDAE; HOMO.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=HEART MUSCLE;			
RX	MEDLINE; 91032031.			
RA	VALLINS W.J., BRAND N.J., DABHADE N., BUTLER-BROWNE G.,			
RA	YACOUB M.H., BARTON P.J.R.;			
RT	"Molecular cloning of human cardiac troponin I using polymerase chain			
RT	reaction."			
RL	FEBS LETT. 270:57-61(1990).			
RN	[2]			
RP	REVISION TO 85, SEQUENCE FROM N.A.			
RX	MEDLINE; 94010323.			
RA	ARMOUR K.L., HARRIS W.J., TEMPEST P.R.;			
RT	"Cloning and expression in Escherichia coli of the cDNA encoding			
RT	human cardiac troponin I."			
RL	GENE 131:287-292(1993).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 92035427.			
RA	HUNKELER N.M., KULLMAN J., MURPHY A.M.;			
RT	"Troponin I isoform expression in human heart."			
RL	CIRC. RES. 69:1409-1414(1991).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 96299735.			
RA	BHAVSAR P.K., BRAND N.J., YACOUB M.H., BARTON P.J.R.;			
RT	"Isolation and characterization of the human cardiac troponin I gene			
RT	(TNNI3)."			
RL	GENOMICS 35:11-23(1996).			
CC	!- FUNCTION: TROPONIN I IS THE INHIBITORY SUBUNIT OF TROPONIN, THE			
CC	THIN FILAMENT REGULATORY COMPLEX WHICH CONFERS CALCIUM-SENSITIVITY			
CC	TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.			
CC	!- TROPONIN I BINDS TO ACTIN-TROPOMYOSIN.			
CC	-----			
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EMBL; X54163; G37428; ALT\_SEQ.  
DR EMBL; M64247; G339967; -.  
DR EMBL; X90780; E196058; -.  
DR EMBL; X90781; E196058; JOINED.  
DR EMBL; X90782; E196058; JOINED.  
DR PIR; A61229; A61229.  
DR MIM; I91044; -.  
DR PFAM; PF00992; Troponin; 1.  
KW MUSCLE PROTEIN; ACTIN-BINDING; ACETYLATION.  
FT INIT\_MET 0 0  
FT MOD\_RES 1 1 ACETYLATION (BY SIMILARITY).  
FT SITE 79 79 INVOLVED IN TNI-TNT INTERACTIONS.  
FT SITE 96 96 INVOLVED IN TNI-TNT INTERACTIONS.  
FT SITE 31 78 INVOLVED IN BINDING TNC.  
FT DOMAIN 128 148 INVOLVED IN BINDING TNC AND ACTIN.  
FT DOMAIN 128 148 INVOLVED IN BINDING TNC AND ACTIN.  
SQ SEQUENCE 209 AA; 23876 MW; 2B55B1B3 CRC32;

Query Match 98.4%; Score 671; DB 1; Length 209;  
Best Local Similarity 100.0%; Pred. No. 1.63e-116;  
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 AGGSSDAAREPRPAPAPIRRRSSNYRAYATEPHAKKSKISASRKLQKLTLLQIAKQEL 60  
QY 2 AGGSSDAAREPRPAPAPIRRRSSNYRAYATEPHAKKSKISASRKLQKLTLLQIAKQEL 61  
Db 61 ERAEEREGKGRALSTRCQPLAGLGFAGLQDLQCRQ 98  
QY 62 ERAEEREGKGRALSTRCQPLAGLGFAGLQDLQCRQ 99

RESULT 2  
ID TRIC\_MOUSE STANDARD; PRT; 210 AA.  
AC P48787;  
DT 01-FEB-1996 (REL. 33, CREATED)  
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)  
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)  
DE TROPONIN I, CARDIAC MUSCLE.  
GN TNN13.  
OS MUS MUSCULUS (MOUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;  
OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.  
RN SEQUENCE FROM N.A.  
RP MEDLINE; 94103233.  
RX AUSONI S., CAMPIONE M., PICARD A., MORETTI P., VITTADELLO M.,  
RA DE NARDI C., SCHIAFFINO S.;  
RT "Structure and regulation of the mouse cardiac troponin I gene."  
RL J. BIOL. CHEM. 269:339-346(1994).  
RN SEQUENCE FROM N.A.  
RP STRAIN-CD-1; TISSUE=HEART;  
RX MEDLINE; 94253083.  
RA GUO X., WATTANAPERMOOL J., PALMITER K.A., MURPHY A.M., SOLARO R.J.;  
RT "Mutagenesis of cardiac troponin I. Role of the unique NH2-terminal peptide in myofibrillar activation."  
RL J. BIOL. CHEM. 269:15210-15216(1994).  
RN FUNCTION: TROPONIN I IS THE INHIBITORY SUBUNIT OF TROPONIN. THE THIN FILAMENT REGULATORY COMPLEX WHICH CONFERS CALCIUM-SENSITIVITY TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.  
CC -!- TROPONIN I BINDS TO ACTIN-TROPOMYOSIN.  
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CC EMBL; Z22784; G313105; -.  
DR EMBL; U09181; G508866; -.  
DR MGI; MGI-98783; TNN13.  
DR PFAM; PF00992; Troponin; 1.  
KW MUSCLE PROTEIN; ACTIN-BINDING; ACETYLATION.  
FT INIT\_MET 0 0  
FT MOD\_RES 1 1 ACETYLATION (BY SIMILARITY).  
FT SITE 80 80 INVOLVED IN TNI-TNT INTERACTIONS.  
FT SITE 97 97 INVOLVED IN TNI-TNT INTERACTIONS.  
FT SITE 32 79 INVOLVED IN BINDING TNC.  
FT DOMAIN 129 150 INVOLVED IN BINDING TNC AND ACTIN.  
SQ SEQUENCE 210 AA; 24127 MW; 14C53199 CRC32;

Query Match 88.4%; Score 603; DB 1; Length 210;  
Best Local Similarity 88.9%; Pred. No. 7.86e-102;  
Matches 88; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

Db 1 ADESSDAAGEPOPAPAPYRRSSNYRAYATEPHAKKSKISASRKLQKLTLLQIAKQ 60  
QY 2 AGGSSDAAREPRPAPAPIRRRSSNYRAYATEPHAKKSKISASRKLQKLTLLQIAKQ 60  
Db 61 MEREAEEREGKGRVLRTRCQPLDGLGFEELQDLQCRQ 99  
QY 61 LEREAEEREGKGRALSTRCQPLAGLGFAGLQDLQCRQ 99

RESULT 3  
ID TRIC\_RAT STANDARD; PRT; 210 AA.  
AC P23693;  
DT 01-NOV-1991 (REL. 20, CREATED)  
DT 01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)  
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)  
DE TROPONIN I, CARDIAC MUSCLE.  
GN TNN13 OR TNI OR CTNI.  
OS RATTUS NORVEGICUS (RAT).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;  
OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.  
RN SEQUENCE FROM N.A.  
RP MEDLINE; 91105162.  
RX MURPHY A.M., JONES L. II, SIMS H.F., STRAUSS A.W.;  
RA "Molecular cloning of rat cardiac troponin I and analysis of troponin I isoform expression in developing rat heart."  
RL BIOCHEMISTRY 30:707-712(1991).  
RN SEQUENCE FROM N.A.  
RP MEDLINE; 92037196.  
RX AUSONI S., DE NARDI C., MORETTI P., GORZA L., SCHIAFFINO S.;  
RT "Developmental expression of rat cardiac troponin I mRNA."  
RL DEVELOPMENT 112:1041-1051(1991).  
RN SEQUENCE FROM N.A.  
RP MEDLINE; 91359315.  
RX MARTIN A.F., ORLOWSKI J.;  
RT "Molecular cloning and developmental expression of the rat cardiac-specific isoform of troponin I."  
RL J. MOL. CELL. CARDIOL. 23:583-588(1991).  
RN SEQUENCE FROM N.A.  
RP MEDLINE; 97218094.  
RX MURPHY A.M., THOMPSON W.R., PENG L.F., JONES L.;  
RT "Regulation of the rat cardiac troponin I gene by the transcription factor GATA-4."  
RL BIOCHEM. J. 322:393-401(1997).  
RN FUNCTION: TROPONIN I IS THE INHIBITORY SUBUNIT OF TROPONIN. THE THIN FILAMENT REGULATORY COMPLEX WHICH CONFERS CALCIUM-SENSITIVITY TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.  
CC -!- TROPONIN I BINDS TO ACTIN-TROPOMYOSIN.  
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Db 57 EREAERRGKGRALSTRCPLELAGLFAELQDLCRQ 94  
|||||

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QY 62 EREAEREGKGRALSTRCOPLEAGLGLFAELQDLQCRQ 99
      6
RESULT
ID TRIC_CORJA STANDARD; PRT; 207 AA.
AC P27572;
DT 01-AUG-1992 (REL. 23, CREATED)
DT 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE TROPONIN I, CARDIAC MUSCLE.
OS COTURNIX COTURNIX JAPONICA (JAPANESE QUAIL).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
OC NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; COTURNIX.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 92011768.
RA HASTINGS K.E., KOPPE R.I., MARMUR E., BADER D., SHIMADA Y.,
RA TOYOTA N.;
RT "Structure and developmental expression of troponin I isoforms. CDNA
RT clone analysis of avian cardiac troponin I mRNA.";
RL J. BIOL. CHEM. 266:19659-19665(1991).
CC -1- FUNCTION: TROPONIN I IS THE INHIBITORY SUBUNIT OF TROPONIN. THE
CC THIN FILAMENT REGULATORY COMPLEX WHICH CONFERS CALCIUM-SENSITIVITY
CC TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.
CC -1- TROPONIN I BINDS TO ACTIN-TROPOMYOSIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L25721; G410051; --
CC DR PFAM: PF00992; Troponin; 1.
CC KW MUSCLE PROTEIN; ACTIN-BINDING.
CC FT INIT_MET 0 0 BY SIMILARITY.
CC FT DOMAIN 9 14 POLY-GLU.
CC FT DOMAIN 17 22 POLY-GLU.
CC FT DOMAIN 84 91 POLY-GLU.
CC SQ SEQUENCE 207 AA; 23470 MW; 4B245E86 CRC32;

Query Match 63.2%; Score 431; DB 1; Length 207;
Best Local Similarity 67.4%; Pred. No. 2.78e-65;
Matches 62; Conservative 12; Mismatches 17; Indels 1; Gaps 1;

Db 1 AEEEPKPPPLRRSSNRYGYVPEPHAKROKISASRKLQKTLKLLQAKRLEREEQE 60
QY 9 AREPRPAPAPRRSS-NRYAYATEPHAKKKSISASRKLQKTLKLLQAKLEERAGEE 67

Db 61 RAGEKQRLGELCPPELDGLGVAQLQELCRE 92
QY 68 RRGKGRALSTRCOPLEAGLGLFAELQDLQCRQ 99

      7
RESULT
ID TRIC_XENLA STANDARD; PRT; 243 AA.
AC P50754;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE TROPONIN I, CARDIAC MUSCLE (TROPONIN IC).
OS XENOPUS LAEVIS (AFRICAN CLAWED FROG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;
OC MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS.
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-HEART MUSCLE;
RX MEDLINE: 95046865.
RA DRYSDALE T.A., TONISSEN K.F., PATTERSON K.D., CRAWFORD M.J.,
RA KRIEG P.A.;
RT "Cardiac troponin I is a heart-specific marker in the Xenopus embryo:

```

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RT expression during abnormal heart morphogenesis.";
RL DEV. BIOL. 165:432-441(1994).
CC -1- FUNCTION: TROPONIN I IS THE INHIBITORY SUBUNIT OF TROPONIN. THE
CC THIN FILAMENT REGULATORY COMPLEX WHICH CONFERS CALCIUM-SENSITIVITY
CC TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.
CC -1- TISSUE SPECIFICITY: HEART.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT ALL STAGES OF DEVELOPMENT.
CC -1- TROPONIN I BINDS TO ACTIN-TROPOMYOSIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L25721; G410051; --
CC DR PFAM: PF00992; Troponin; 1.
CC KW MUSCLE PROTEIN; ACTIN-BINDING.
CC FT INIT_MET 0 0 BY SIMILARITY.
CC FT DOMAIN 9 14 POLY-GLU.
CC FT DOMAIN 17 22 POLY-GLU.
CC FT DOMAIN 84 91 POLY-GLU.
CC SQ SEQUENCE 243 AA; 28067 MW; 12B17823 CRC32;

Query Match 62.9%; Score 429; DB 1; Length 243;
Best Local Similarity 60.0%; Pred. No. 7.28e-65;
Matches 60; Conservative 23; Mismatches 16; Indels 1; Gaps 1;

Db 24 VAPEPKPAPPAPPLRRSSNRYAYATEPOVKRPKISASRKLQKTLKLLQAKIAK 83
QY 1 MADGSDAREPRPAPAPRRSS-NRYAYATEPHAKKKSISASRKLQKTLKLLQAKIAK 99

Db 84 EMREERERAREKERYLAEHCPQLGSLRSLEQLDQCE 123
QY 60 ELEREAEREGKGRALSTRCOPLEAGLGLFAELQDLQCRQ 99

      8
RESULT
ID TRIC_CHICK STANDARD; PRT; 168 AA.
AC P27673;
DT 01-AUG-1992 (REL. 23, CREATED)
DT 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
DT 01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)
DE TROPONIN I, CARDIAC MUSCLE (FRAGMENT).
OS GALLUS GALLUS (CHICKEN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
OC NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 92011768.
RA HASTINGS K.E., KOPPE R.I., MARMUR E., BADER D., SHIMADA Y.,
RA TOYOTA N.;
RT "Structure and developmental expression of troponin I isoforms. CDNA
RT clone analysis of avian cardiac troponin I mRNA.";
RL J. BIOL. CHEM. 266:19659-19665(1991).
CC -1- FUNCTION: TROPONIN I IS THE INHIBITORY SUBUNIT OF TROPONIN. THE
CC THIN FILAMENT REGULATORY COMPLEX WHICH CONFERS CALCIUM-SENSITIVITY
CC TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.
CC -1- TROPONIN I BINDS TO ACTIN-TROPOMYOSIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M73703; G212821; --
CC DR PFAM: PF00992; Troponin; 1.
CC KW MUSCLE PROTEIN; ACTIN-BINDING.

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OS      HOMO SAPIENS (HUMAN).
OC      EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC      PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
[1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE; 90307007.
RA      WADE R., EDDY R., SHOWS T.B., KEDES L.;
RT      "CDNA sequence, tissue-specific expression, and chromosomal mapping
RL      of the human slow-twitch skeletal muscle isoform of troponin I.";
RN      GENOMICS 7:346-357(1990).
[2]
RP      SEQUENCE FROM N.A.
RX      TISSUE-BLOOD;
RC      MEDLINE; 94193765.
RA      CORIN S.J., JUHASZ O., ZHU L., CONLEY P.J., KEDES L., WADE R.;
RT      "Structure and expression of the human slow twitch skeletal muscle
RL      troponin I gene.";
RN      J. BIOL. CHEM. 269:10651-10659(1994).
CC      -!- THIN FILAMENT REGULATORY COMPLEX WHICH CONFERS CALCIUM-SENSITIVITY
CC      TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.
CC      -!- TROPONIN I BINDS TO ACTIN-TROPOMYOSIN.
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CC      or send an email to license@isb-sib.ch).
-----
CC      EMBL; J04760; G339965; .
DR      EMBL; L21910; G437009; -.
DR      EMBL; L21906; G437009; JOINED.
DR      EMBL; L21908; G437009; JOINED.
DR      EMBL; L21909; G437009; JOINED.
DR      PIR; A35355; A35355.
DR      MIM; 191042; -.
DR      PFAM; PF00992; Troponin; 1.
DR      MUSCLE PROTEIN; ACTIN-BINDING.
FT      INIT-MET          0
FT      DOMAIN           1  47   INVOLVED IN BINDING TNC.
FT      DOMAIN           96  117  INVOLVED IN BINDING TNC AND ACTIN.
FT      CONFLICT         181  182   KS -> NA (IN REF. 1).
SQ      SEQUENCE        186 AA;  21561 MW;  5DABD050 CRC32;
Query Match       33.9%; Score 231; DB 1; Length 186;
Best Local Similarity 50.7%; Pred. No. 7.12e-25;
Matches    34; Conservative 14; Mismatches 19; Indels 0; Gaps 0;

Db      1 PEVERPKPTASRKLKLLSLAKAKECEWEOEHEERAEKVYLAERIPLQTRGLSLA 60
| :||:||||| ||::| |::| ||| ||| |::| |::| |::|
QY     33 PHAKKSISASRKQLTKLTLLQIAKLEAREABERGEGKRALSTROCPLELAGLGFAE 92
| :||:||||| |||||
Db      61 LDLCRE 67
| :||:|||
QY     93 LDLCRQ 99
| :||:|||

RESULT 11
ID      TRIS_RABIT STANDARD; PRT; 184 AA.
AC      P02645;
DT      21-JUL-1986 (REL. 01, CREATED)
DT      21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT      01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE      TROPONIN I, SLOW SKELETAL MUSCLE (TROPONIN I, SLOW-TWITCH ISOFORM).
GN      TNNT1.
OS      ORCTOLOGUS CUNICULUS (RABBIT).
OC      EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC      LAGOMORPHA; LEPORIDAE; ORICTOLAGUS.
[1]
RP      SEQUENCE.
RX      MEDLINE; 78060292.
```

GRAND R.J.A., WILKINSON J.M.;  
RT "The amino acid sequence of rabbit slow-muscle troponin I.";  
RT BIOCHEM. J. 167:183-192(1977).  
CC -I- FUNCTION: TROPONIN I IS THE INHIBITORY SUBUNIT OF TROPONIN, THE  
CC THIN FILAMENT REGULATORY COMPLEX WHICH CONFERS CALCIUM-SENSITIVITY  
CC TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.  
CC -I- TROPONIN I BINDS TO ACTIN-TROPOMIOSIN.  
DR FIR; A03089; TPRBIW.  
DR PFAM; PFO0992; Troponin; 1.  
KW MUSCLE PROTEIN; ACTIN-BINDING.  
FT MOD\_RES 1 1 BLOCKED (IN 25% OF THE CHAINS).  
FT VARIANT 183 184 MISSING (IN SOME MOLECULES).  
FT DOMAIN 1 45 INVOLVED IN BINDING TNC.  
FT DOMAIN 94 115 INVOLVED IN BINDING TNC AND ACTIN.  
SQ SEQUENCE 184 AA; 21143 MW; 49043E2D CRC32;

Query Match 32.1%; Score 219; DB 1; Length 184;  
Best Local Similarity 52.2%; Pred. No. 1.36e-22;  
Matches 35; Conservative 13; Mismatches 17; Indels 2; Gaps

Db 1 PEVERSKITASRKL-LKSLMLAKAK-ECQOPEHREAREKVKYLAERIPALQTRGLSLSA 58  
I :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
QY 33 PHAKKSKISASRKLQKLTLIIQIAQELEREAEERGEKGRALSTRCPLELAGLGF 92  
|||  
Db 59 LQDLCRQ 65  
|||||  
QY 93 LQDLCRQ 99  
|||||

RESULT 12

ID TRIF\_RABIT STANDARD; PRT; 181 AA.  
AC P02643;  
DT 21-JUL-1986 (REL. 01, CREATED)  
DT 01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)  
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)  
DE TROPONIN I, FAST SKELETAL MUSCLE (TROPONIN I, FAST-TWITCH ISOFORM).  
GN TNM2.  
OS ORYCTOLAGUS CUNICULUS (RABBIT).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;  
OC LAGOMORPHA; LEPORIDAE; ORYCTOLAGUS.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 93094259.  
RA SHENG Z., PAN B.S., MILLER T., POTTER J.D.;  
RT "Isolation, expression, and mutation of a rabbit skeletal muscle cDNA  
RT clone for troponin I. The role of the NH2 terminus of fast skeletal  
RT muscle troponin I in its biological activity.";  
RT J. BIOL. CHEM. 267:25407-25413(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=MUSCLE;  
RX MEDLINE; 94227244.  
RA WU Q.L., RAYCHOWDHURY M.K., DU Y., JHA P.K., LEAVIS P.C., SARKAR S.;  
RT "Characterization of a rabbit fast skeletal troponin I cDNA: a  
RT comparative sequence analysis of vertebrate isoforms and tissue-  
RT specific expression of a single copy gene.";  
RN DNA SEQ. 4:113-121(1993).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 93265949.  
RA KLWNE L., MAEDA K., MAEDA Y.;  
RT "E. coli expression and characterization of a mutant troponin I with  
RT the three cysteine residues substituted.";  
RN FEBS LETT. 323:83-88(1993).  
RN [4]  
RP SEQUENCE.  
RX MEDLINE; 76039510.  
RA WILKINSON J.M., GRAND R.J.A.;  
RT "The amino acid sequence of troponin I from rabbit skeletal muscle.";  
RN BIOCHEM. J. 149:493-496(1975).  
RN [5]  
RP REVISION.  
RX MEDLINE; 78114026.

WILKINSON J.M., GRAND R.J.A.;  
"Comparison of amino acid sequence of troponin I from different striated muscles";  
NATURE 271:31-35(1978).  
[6]  
SEQUENCE OF 1-24 AND 165-177 FROM N.A.  
MEDLINE; 83167564.  
RX PUTNEY S.D., HERLIHY W.C., SCHIMMEL P.R.;  
"A new troponin T and cDNA clones for 13 different muscle proteins, found by shotgun sequencing";  
NATURE 302:718-721(1983).  
[7]  
PHOSPHORYLATION SITES.  
RX MEDLINE; 74309023.  
RX MOIR A.J.G., WILKINSON J.M., PERRY S.V.;  
"The phosphorylation sites of troponin I from white skeletal muscle of the rabbit";  
FEBS LETT. 42:253-256(1974).  
[8]  
PHOSPHORYLATION SITES.  
RX MEDLINE; 74308154.  
RX HUANG T.S., BYLUND D.B., STULL J.T., KREBS E.G.;  
"The amino acid sequences of the phosphorylated sites in troponin-I from rabbit skeletal muscle";  
FEBS LETT. 42:249-252(1974).  
[9]  
X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 1-47 IN COMPLEX WITH TNC.  
RX MEDLINE; 98226730.  
RX VASSILIEV D.G., TAKEDA S., WAKATSUKI S., MAEDA K., MAEDA Y.;  
"Crystal structure of troponin C in complex with troponin I fragment at 2.3-A resolution";  
PROC. NATL. ACAD. SCI. U.S.A. 95:4847-4852(1998).  
CC -!- FUNCTION: TROPONIN I IS THE INHIBITORY SUBUNIT OF TROPONIN, THE THIN FILAMENT REGULATORY COMPLEX WHICH CONFERS CALCIUM-SENSITIVITY TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.  
CC -!- TROPONIN I BINDS TO ACTIN-TROPOMYOSIN.  
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CC EMBL; I04347; G165778; -  
DR EMBL; X14190; G508473; -  
DR EMBL; S61403; G409009; -  
DR EMBL; V00897; G1737; -  
DR EMBL; V00898; G929767; -  
DR PIR; A03087; TPRBJ5.  
DR PDB; 1A2X; 15-JUL-98.  
DR PFM; PFC00992; Troponin; 1.  
KW MUSCLE PROTEIN; ACETYLATION; PHOSPHORYLATION; ACTIN-BINDING;  
KW 3D-STRUCTURE.  
KW INIT\_MET 0 0  
FT MOD\_RES 1 1  
FT MOD\_RES 11 11  
FT MOD\_RES 117 117  
FT DOMAIN 1 47  
FT DOMAIN 96 116  
FT CONFLICT 153 155  
FT CONFLICT 181 AA; 21083 MW; OAC30953 CRC32;  
SQ SEQUENCE 181 AA; 30.5%; Score 208; DB 1; Length 181;  
Query Match  
Best Local Similarity 42.9%;  
Matches 27; Conservative 19; Mismatches 16; Indels 1; Gaps 1;  
  
Db 5 KRNRATARQHLKSVMLQTAATELEKGRRAEAEKONYLAECPPPLSLPG-SMAEYQEL 63  
IQY 37 KKSISASRKLQKTLUQIAKQELERAEERKGRALSTRCPQLEAGLFAELQDL 96  
Db 64 CKO 66



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QY 97 CRQ 99

RESULT 13
ID TRIF_MOUSE STANDARD; PRT; 181 AA.
AC P13412;
DT 01-JAN-1990 (REL. 13, CREATED)
DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE TROPONIN I, FAST SKELETAL MUSCLE (TROPONIN I, FAST-TWITCH ISOFORM).
GN TNNI2.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89340548.
RA KOPPE R.I., HALLAUER P.L., KARPATI G., HASTINGS K.E.M.;
RT "cDNA clone and expression analysis of rodent fast and slow skeletal
muscle troponin I mRNAs."
RJ J. BIOL. CHEM. 264.14327-14333(1989).
CC -|- FUNCTION: TROPONIN I IS THE INHIBITORY SUBUNIT OF TROPONIN, THE
THIN FILAMENT REGULATORY COMPLEX WHICH CONFERS CALCIUM-SENSITIVITY
CC TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.
CC -|- TROPONIN I BINDS TO ACTIN-TROPOMYOSIN.
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CC -----
CC EMBL; J04992; G202165;
CC PIR; A44786; A44786.
CC MGD; MGI:105070; TNNI2.
CC PFAM; PF00992; Troponin; 1.
CC HSP; P02643; IA2X.
CC MUSCLE PROTEIN; ACTIN-BINDING.
FT INIT_MET 0 0
FT DOMAIN 1 47 INVOLVED IN BINDING TNC.
FT DOMAIN 96 116 INVOLVED IN BINDING TNC AND ACTIN.
SQ SEQUENCE 181 AA; 21226 MW; BB5D5B61 CRC32;

Query Match 30.1%; Score 205; DB 1; Length 181;
Best Local Similarity 41.3%; Pred. No. 5.81e-20;
Matches 26; Conservative 20; Mismatches 16; Indels 1; Gaps 1;

Db 5 KRNRATARQHLKSVMLQIAATELEKESRESEKENYLSEHCPLPHIPG-SMSEVOEL 63
QY 37 KKSISASRKLQTLTLLQIAKQELERAEERGERKGRALSTRCOPLAGLGFALQDL 96
Db 64 CKQ 66
QY 97 CRQ 99

RESULT 14
ID TRIF_RAT STANDARD; PRT; 181 AA.
AC P27768;
DT 01-AUG-1992 (REL. 23, CREATED)
DT 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE TROPONIN I, FAST SKELETAL MUSCLE (TROPONIN I, FAST-TWITCH ISOFORM).
GN TNNI2 OR TRP1.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
RN [1]
RP SEQUENCE FROM N.A.
RX GRAVEL M., HASTINGS K.E.;

SUBMITTED (XXX-1991) TO EMBL/GENBANK/DBJ DATA BANKS.
-|- FUNCTION: TROPONIN I IS THE INHIBITORY SUBUNIT OF TROPONIN, THE
THIN FILAMENT REGULATORY COMPLEX WHICH CONFERS CALCIUM-SENSITIVITY
TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.
-|- TROPONIN I BINDS TO ACTIN-TROPOMYOSIN.
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-----
EMBL; M73701; G206985;
PFAM; PF00992; Troponin; 1.
HSP; P02643; IA2X.
MUSCLE PROTEIN; ACTIN-BINDING.
FT INIT_MET 0 0 BY SIMILARITY.
FT DOMAIN 1 47 INVOLVED IN BINDING TNC.
FT DOMAIN 96 116 INVOLVED IN BINDING TNC AND ACTIN.
SQ SEQUENCE 181 AA; 21197 MW; DDDFEA8 CRC32;

Query Match 29.8%; Score 203; DB 1; Length 181;
Best Local Similarity 41.3%; Pred. No. 1.37e-19;
Matches 26; Conservative 20; Mismatches 16; Indels 1; Gaps 1;

Db 5 KRNRATARQHLKSVMLQIAATELEKESRESEKENYLSEHCPLPHIPG-SMSEVOEL 63
QY 37 KKSISASRKLQTLTLLQIAKQELERAEERGERKGRALSTRCOPLAGLGFALQDL 96
Db 64 CKQ 66
QY 97 CRQ 99

RESULT 15
ID TRIF_HUMAN STANDARD; PRT; 181 AA.
AC P48788;
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE TROPONIN I, FAST SKELETAL MUSCLE (TROPONIN I, FAST-TWITCH ISOFORM).
GN TNNI2.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-SKELETAL MUSCLE;
RX MEDLINE; 94198300.
RA ZHU L., PEREZ-ALVARADO G., WADE R.;
RT "Sequencing of a cDNA encoding the human fast-twitch skeletal muscle
isoform of troponin I."
RL BIOCHIM. BIOPHYS. ACTA 1217:338-340(1994).
CC -|- FUNCTION: TROPONIN I IS THE INHIBITORY SUBUNIT OF TROPONIN, THE
THIN FILAMENT REGULATORY COMPLEX WHICH CONFERS CALCIUM-SENSITIVITY
TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.
CC -|- TROPONIN I BINDS TO ACTIN-TROPOMYOSIN.
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EMBL; L21715; G452078;
PFAM; PF00992; Troponin; 1.
HSP; P02643; IA2X.
MUSCLE PROTEIN; ACTIN-BINDING.
```

FT INIT\_MET 0 0 BY SIMILARITY.  
FT DOMAIN 1 47 INVOLVED IN BINDING TNC.  
FT DOMAIN 96 116 INVOLVED IN BINDING TNC AND ACTIN.  
SQ SEQUENCE 181 AA; 21207 MW; 83ED65E4 CRC32;  
Query Match 29.5%; Score 201; DB 1; Length 181;  
Best Local Similarity 39.7%; Pred. No. 3.22e-19;  
Matches 25; Conservative 21; Mismatches 16; Indels 1; Gaps 1;  
Db 5 KNRATARRQHLSVMLQIAATELEKEESRRFAEKONYLAETHCPPLHIPG-SMSEVOEL 63  
QY 37 KRSKISASRKLQKTLLELQIAKQELERAEERGERGKRALSTRCPLELAGLGFALQDL 96  
Db 64 CKQ 66  
QY 97 CRQ 99

Search completed: Fri Jan 21 14:28:03 2000  
Job time : 20 secs.